


```

;
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; Reagents
;
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/671,658A
; FILING DATE: 27-Sep-2000
; CLASSIFICATION: <unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-671-658A-2

Query Match          99.6%; Score 1554; DB 5; Length 316;
Best Local Similarity 99.7%; Pred. No. 7.9e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVPHEGPLHPAPAPAPAPPAASRSMFLALLGLGLGVCSIALFLYFRAQMPNRISE 60
    |||||||
Db 23 GVPHEGPLHPAPAPAPAPPAASRSMFLALLGLGLGVCSIALFLYFRAQMPNRISE 82

QY 61 DSTHCFYILRLHFNADLQDSTLESEDTLPDSCRRMKAFOGAVOKELQHTVGPQRESGA 120
    |||||||
Db 83 DSTHCFYILRLHFNAGLQDSTLESEDTLPDSCRRMKAFOGAVOKELQHTVGPQRESGA 142

QY 121 PAMMGSLDVAQQRKPPAOPFAHLTTINAASIPSGSHKVTLSWYHDSGMKISNMTLSN 180
    |||||||
Db 143 PAMMGSLDVAQQRKPPAOPFAHLTTINAASIPSGSHKVTLSWYHDSGMKISNMTLSN 202

QY 181 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMYVYVTKTSIKIPSSHNLMKGSTKN 240
    |||||||
Db 203 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMYVYVTKTSIKIPSSHNLMKGSTKN 262

QY 241 WSGNSEHFHYSINVGGFKRLRAGEEISIQVSNPSILDDPDQATYFGAFKVDID 294
    |||||||
Db 263 WSGNSEHFHYSINVGGFKRLRAGEEISIQVSNPSILDDPDQATYFGAFKVDID 316

RESULT 3
US-10-105-057-2
; Sequence 2, Application US/10105057
; GENERAL INFORMATION:
; APPLICANT: Barnes-Jewish Hospital, d/b/a The Jewish Hospital of St. Louis
```

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;
; TITLE OF INVENTION: STIMULATION OF OSTEOGENESIS USING RANK LIGAND FUSION PROTEINS
; FILE REFERENCE: BCH 10054.1
; CURRENT APPLICATION NUMBER: US/10/105,057
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/277,855
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mus musculus
;
US-10-105-057-2

Query Match          99.6%; Score 1554; DB 6; Length 316;
Best Local Similarity 99.7%; Pred. No. 7.9e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVPHEGPLHPAPAPAPPAASRSMFLALLGLGLGVCSIALFLYFRAQMPNRISE 60
    |||||||
Db 23 GVPHEGPLHPAPAPAPPAASRSMFLALLGLGLGVCSIALFLYFRAQMPNRISE 82

QY 61 DSTHCFYILRLHFNADLQDSTLESEDTLPDSCRRMKAFOGAVOKELQHTVGPQRESGA 120
    |||||||
Db 83 DSTHCFYILRLHFNAGLQDSTLESEDTLPDSCRRMKAFOGAVOKELQHTVGPQRESGA 142

QY 121 PAMMGSLDVAQQRKPPAOPFAHLTTINAASIPSGSHKVTLSWYHDSGMKISNMTLSN 180
    |||||||
Db 143 PAMMGSLDVAQQRKPPAOPFAHLTTINAASIPSGSHKVTLSWYHDSGMKISNMTLSN 202

QY 181 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMYVYVTKTSIKIPSSHNLMKGSTKN 240
    |||||||
Db 203 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMYVYVTKTSIKIPSSHNLMKGSTKN 262

QY 241 WSGNSEHFHYSINVGGFKRLRAGEEISIQVSNPSILDDPDQATYFGAFKVDID 294
    |||||||
Db 263 WSGNSEHFHYSINVGGFKRLRAGEEISIQVSNPSILDDPDQATYFGAFKVDID 316

RESULT 4
PCT-US02-16002-10
; Sequence 10, Application PC/TUS0216002
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: DOUGALX, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-WO
; CURRENT APPLICATION NUMBER: PCT/US02/16002
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
;
PCT-US02-16002-10

Query Match          85.0%; Score 1326.5; DB 1; Length 317;
Best Local Similarity 84.5%; Pred. No. 2.2e-111;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

QY 1 GVPHEGPLHPAPAPAPPAASRSMFLALLGLGLGVCSIALFLYFRAQMPNRISE 60
    |||||||
Db 23 GVPHEGPLHPAPAPPAQPPAASRSMFLALLGLGLGVCSIALFLYFRAQMPNRISE 81

QY 61 DSTHCFYILRLHFNADLQDSTLESEDTLPDSCRRMKAFOGAVOKELQHTVGPQRESGA 118
    |||||||
Db 82 DSTHCFYILRLHFNADLQDSTLESEDTLPDSCRRMKAFOGAVOKELQHTVGPQRESGA 141
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Query Match 14.9%: Score 232: DB 5: Length 246;
Best Local Similarity 25.0%: Pred. No. 3.9e-13;
Matches 69: Conservative 53: Mismatches 108: Indels 46: Gaps 8;

QY 21 PAASHSMFLALGLGAGVCSIALFFFRAMD--PNRISDSYHCFYRLRLHENDL 78
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 10 PSLGTCVLIVIFYVLLDLSLCVAAYVYFTNLKMKODKYSKSGTACF-----LLEDSSY 64

QY 79 QDSTLESDTLPDSCRKKAQFOGAVORELOHIVGPRFSGAPAMEGSMLDVAORQPE 138
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 65 WDP--NDEESNMSPCMQVKWQDLRQLVRLMLRT----- 95

QY 139 AOPFHLITMAAIPSGSHK---TLSSWYHDR-GWAKISNKTLSNGKLRVNOGDFYLL 194
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 96 ----SEETISYVQ-DSKNEKALGRKINMESRSRSHSLNLHLNGETLVHKEKGYIT 150

QY 195 ANICPRHHETGGSVPTDQLQMLVYVVKRSIKIPSSHNLMLKGGSTYNNAGNSSEHFHYSTNV 254
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 151 SQYFRFOEETKENTKKNQKQWQYLYTKT-SYDPDILLMKSAKRNCSKWDKDEYGLSYIQ 209

QY 255 GGFELRAGEELSIQVSNPSLLDPQODVTFYGAFFV 290
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 210 GGIFELKENDRIPLVSYVNEHLIDMDHEASFFGAFLLV 245

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RESULT 11
US-09-900-530A-10
: Sequence 10, Application US/09900530A
: GENERAL INFORMATION:
: APPLICANT: Seol, Dae-Wu
: APPLICANT: Billiar, Timothy R.
: TITLE OF INVENTION: DNA Cassette for the Production of
: TITLE OF INVENTION: Secretable Recombinant Trimeric Tral Proteins, Tetracycline
: TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their
: TITLE OF INVENTION: Combination and Use in Gene Therapy
: FILE REFERENCE: 5006-1-002
: CURRENT APPLICATION NUMBER: US/09/900,530A
: CURRENT FILING DATE: 2002-03-19
: PRIOR APPLICATION NUMBER: KR 2000-38441
: PRIOR FILING DATE: 2000-07-06
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 168
: TYPE: PR1
: ORGANISM: homo sapiens
: US-09-900-530A-10

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Query Match 14.8% Score 230.5; DB 5; Length 168;
Best Local Similarity 33.5%; Pred. No. 3.2e-13;
Matches 57; Conservative 32; Mismatches 68; Indels 13; Gaps 5;

QY 131 VAQGRKPEAPFAHL-----INAAISPGSHKVTL-----SSWYHDR-GNAKISNMTLN 180
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1 VRRGRGQRAVA-AHITGRGRSNTLTSSPNSKNEKALGKIKSMSSSSSGISFLNLHRLN 58
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 181 GKLRVADGFFYLIVANICFRHHETSGSVPTDYLQLMVYVNTSTIKIPSSHNLMKGSGTKN 240
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 59 GELVIVHEKGFYIYSOTYFRFQEEIKETMTKDKQWQVIYKYT-SYDDPLILMKSRANSC 117
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 241 WSGNSEHFYSINVGGEFLRAGEISIQVSNPSLSDPPDQATFECAFV 290
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 118 WSDADETGLTSLYOGGIEFLKENDIIFVSYNEHLIDMDHASEGFAFLV 167
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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1  APPLICANT:  Marsters, Scott A.
2  APPLICANT:  Pletti, Robert M.
3  APPLICANT:  Wood, William
4  TITLE OF INVENTION:  NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
5  TITLE OF INVENTION:  NUCLEIC
6  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
7  FILE REFERENCE:  P1206R1
8  CURRENT APPLICATION NUMBER:  US/10/116,378
9  CURRENT FILING DATE:  2002-04-04
10 PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  09/247,225
11 PRIOR FILING DATE:  EARLIER FILING DATE:  1999-02-09
12 PRIOR APPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  US 60/074,087
13 PRIOR FILING DATE:  EARLIER FILING DATE:  1998-02-09
14 NUMBER OF SEQ ID NOS:  31
15 SEQ ID NO 29
16 LENGTH:  164
17 TYPE:  PRN
18 ORGANISM:  Homo sapiens
19 US-10-116-378-29

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| | | | | |
|-----------------------|-------|--------------------|--------|----------------|
| Query Match | 14.1% | Score 220.5: | DB 6, | Length 164; |
| Best Local Similarity | 30.3% | Pred. No. 2.5e-12; | | |
| Matches | 57; | Conservative | 32; | Mismatches 64; |
| | | | Indels | 35; |
| | | | Gaps | 5 |

```

QY 113 GPARSGAPAMEGSMIDVADGRKPEAPFNLH-----IQAASIPGSHKVTL-----SS 163
Db 1 GPARVA-----AHIGTGRGRNTLSSPSKSKNEKALGRKINS 36

QY 164 WYHDR-CAKATISNMTLSNGKLRVADNGFYLYLVANICFRNHETSGSVPTDYLDLWVYVKT 222
Db 37 WESSRSGHSEFSLNHLRNGELVIEHEKFFYYLYTSQYPRFOEIKENTKNDKQWYLYKY 96

QY 223 SIKLPSHNLMLKGGSTKNMGSNSFHHYLSIVGCFKLRAGEELSTIVSNPSLDDPQDA 262
Db 97 T-SYDPDPLMLKSARNSCWSKDAEYGLYSYOCGIFELKENDRIEYAVTNEDLIDMDEA 155

QY 283 TYFGAFKY 290
Db 156 SFGAFGLY 163

```

```

RESULT 13
US-10-119-480-82
; Sequence 82: Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 82
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-119-480-82

```

```

RESULT 12
US-10-116-378-29
; Sequence 29, Application US/10116378
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
;
; ORGANISM: Homo Sapien
US-10-119-480-82
Query Match 11.38; Score 176; DB 6; Length 95;
Best Local Similarly 55.4%; Pred. NO. 1.2e-08;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

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Tue Jul 9 13:21:01 2002

us-09-865-363-11.rapn

Page 7

Db 215 NSKYPQDLYMME-GKMSYCTTGOMMARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQ 273
Oy 283 TYFGAFKV 290
Db 274 TFFGLYKL 281

Search completed: July 8, 2002, 19:54:09.
Job time: 12488 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 20:06:01 ; Search time 4715.96 Seconds

(without alignments)
7232.940 Million cell updates/sec

Title: US-09-865-363-10

Perfect score: 1630
Sequence: 1 CCGCGCTCCACACGAGCGT.....TAACCTAATAGAGCTTCAG 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GeneB1: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
|------------|-------|-------------|--------|-------|-------------|

| | | | | | | |
|----|--------|-------|--------|----|------------|--------------------|
| 1 | 1630 | 100.0 | 1630 | 6 | AR156433 | AR156433 Sequence |
| 2 | 1630 | 100.0 | 1630 | 6 | AR164147 | AR164147 Sequence |
| 3 | 1630 | 100.0 | 1630 | 6 | AX147987 | AX147987 Sequence |
| 4 | 1630 | 100.0 | 2225 | 10 | AF019048 | AF019048 Mus muscu |
| 5 | 1628.4 | 99.9 | 2225 | 6 | AK062119 | AK062119 Sequence |
| 6 | 1628.4 | 99.9 | 2229 | 10 | AF053713 | AF053713 Mus muscu |
| 7 | 1615.8 | 99.1 | 2191 | 6 | AR157058 | AR157058 Sequence |
| 8 | 1615.8 | 99.1 | 2191 | 6 | AX140162 | AX140162 Sequence |
| 9 | 1588.2 | 97.4 | 2237 | 10 | AF013170 | AF013170 Mus muscu |
| 10 | 1152.4 | 70.7 | 2029 | 6 | E34349 | E34349 DNA and pro |
| 11 | 1152.4 | 70.7 | 2029 | 10 | AB022036S4 | AB022036 Mus muscu |
| 12 | 939.6 | 57.6 | 2271 | 9 | AF053712 | AF053712 Homo sapl |
| 13 | 928.6 | 57.0 | 2201 | 9 | AF019047 | AF019047 Homo sapl |
| 14 | 885.4 | 54.3 | 951 | 6 | E34350 | E34350 DNA and pro |
| 15 | 885.4 | 54.3 | 951 | 6 | E34388 | E34388 Novel prote |
| 16 | 885.4 | 54.3 | 951 | 10 | AB008426 | AB008426 Mus muscu |
| 17 | 885.4 | 54.3 | 951 | 10 | AB036798 | AB036798 Mus muscu |
| 18 | 843.2 | 51.7 | 2390 | 6 | AX201362 | AX201362 Sequence |
| 19 | 832.8 | 51.1 | 1823 | 9 | AF013171 | AF013171 Homo sapl |
| 20 | 816.6 | 50.1 | 864 | 10 | AB032771 | AB032771 Homo sapl |
| 21 | 773.4 | 47.4 | 957 | 10 | AF187319 | AF187319 Mus muscu |
| 22 | 724.4 | 44.4 | 754 | 10 | AB032772 | AB032772 Mus muscu |
| 23 | 653.6 | 40.1 | 113451 | 2 | AC023287 | AC023287 Homo sapl |
| 24 | 653.6 | 40.1 | 200724 | 9 | AL139382 | AL139382 Human DNA |
| 25 | 618.4 | 37.9 | 809 | 10 | AF425669 | AF425669 Rattus no |
| 26 | 615 | 37.7 | 954 | 6 | AR156434 | AR156434 Sequence |
| 27 | 615 | 37.7 | 954 | 6 | AR164148 | AR164148 Sequence |
| 28 | 615 | 37.7 | 954 | 6 | AX147989 | AX147989 Sequence |
| 29 | 615 | 37.7 | 1034 | 9 | AB064269 | AB064269 Homo sapl |
| 30 | 588.8 | 36.1 | 972 | 9 | AB064270 | AB064270 Homo sapl |
| 31 | 584.2 | 35.8 | 911 | 9 | AB061227 | AB061227 Homo sapl |
| 32 | 556.8 | 34.2 | 818 | 9 | AB064268 | AB064268 Homo sapl |
| 33 | 547.4 | 33.6 | 930 | 9 | AB037599 | AB037599 Homo sapl |
| 34 | 475.2 | 29.2 | 123551 | 2 | AC094149 | AC094149 Rattus no |
| 35 | 466 | 28.6 | 522 | 6 | AX232589 | AX232589 Sequence |
| 36 | 165.8 | 10.2 | 468 | 6 | E34347 | E34347 DNA and pro |
| 37 | 165.8 | 10.2 | 468 | 10 | AB022037 | AB022037 Mus muscu |
| 38 | 159.4 | 9.8 | 764 | 10 | AB022036S1 | AB022036 Mus muscu |
| 39 | 157.8 | 9.7 | 2026 | 6 | E34346 | E34346 DNA and pro |
| 40 | 130 | 8.0 | 123551 | 2 | AC094149 | AC094149 Rattus no |
| 41 | 105.8 | 6.5 | 575 | 6 | E34348 | E34348 DNA and pro |
| 42 | 105.8 | 6.5 | 575 | 10 | AB022036S3 | AB022038 Mus muscu |
| 43 | 97 | 6.0 | 161835 | 2 | AC104794 | AC104794 Homo sapl |
| 44 | 97 | 6.0 | 190748 | 9 | AC010969 | AC010969 Homo sapl |
| 45 | 91.4 | 5.6 | 2460 | 5 | AF250041 | AF250041 Dario rer |

ALIGNMENTS

| RESULT | 1 | 1630 bp | DNA | 1linear | PAT 08-AUG-2001 |
|------------|--|-------------|-----|---------|-----------------|
| LOCUS | AR156433 | | | | |
| DEFINITION | Sequence 10 from patent US 6242213. | | | | |
| ACCESSION | AR156433 | | | | |
| VERSION | AR156433.1 | GI:15125137 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | 1 (bases 1 to 1630) | | | | |
| AUTHORS | Anderson,D.M. | | | | |
| TITLE | Isolated DNA molecules encoding RANK-L | | | | |
| JOURNAL | Patent: US 6242213-A 10 05-JUN-2001; | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1. 1630 | | | | |
| BASE COUNT | 436 a 355 c 379 g 460 t | | | | |
| ORIGIN | /organism="unknown" | | | | |

| | | | | |
|-----------------------|---------|--------------|-------|--------------|
| Query Match | 100.0% | Score 1630; | DB 6; | Length 1630; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |

| | Matches | 1630: | Conservative | 0: | Mismatches | 0: | Indels | 0: | Gaps | 0: |
|----|---------|--|--------------|----|------------|----|--------|----|------|----|
| Qy | 1 | CCGGGCTCCACACAGAGGGTCCGCTGACACCCCGGCTTTCTCACCGGCTCCGGCGCCG | 60 | | | | | | | |
| Db | 1 | CCGGGCTCCACACAGAGGGTCCGCTGACACCCCGGCTTTCTCACCGGCTCCGGCGCCG | 60 | | | | | | | |
| Qy | 61 | CACCCGCGCCCTCCCGGTCACATGTTCCAGGGCTCTCTGGGGGTGGGAGTGGGCGAGGTG | 120 | | | | | | | |
| Db | 61 | CACCCGCGCCCTCCCGGTCACATGTTCTCTGGGGGTGGGAGTGGGCGAGGTG | 120 | | | | | | | |
| Qy | 121 | TCTGCAGCATGCTCTGTGTTCTGTACTTTCAGGCGCAGATGGATCCTTAACAATATCAG | 180 | | | | | | | |
| Db | 121 | TCTGCAGCATGCTCTGTGTTCTGTACTTTCAGGCGCAGATGGATCCTTAACAATATCAG | 180 | | | | | | | |
| Qy | 181 | AAGACAGCATCTACATGCTTTTATGAATCCCTAGAGCTCATAAAAAGCAGATTTTCAG | 240 | | | | | | | |
| Db | 181 | AAGACAGCATCTACATGCTTTTATGAATCCCTAGAGCTCATAAAAAGCAGATTTTCAG | 240 | | | | | | | |
| Qy | 241 | ACTGCATCTGAGAGTGAAGACACACTACCTGACTCTCTGACAGAGAGATGAACAACGCT | 300 | | | | | | | |
| Db | 241 | ACTGCATCTGAGAGTGAAGACACACTACCTGACTCTCTGACAGAGAGATGAACAACGCT | 300 | | | | | | | |
| Qy | 301 | TTTCAGGGGCGCTGCAGAAAGAACTGCAACACATTTGGGGCCACAGCGCTTCTCAGAG | 360 | | | | | | | |
| Db | 301 | TTTCAGGGGCGCTGCAGAAAGAACTGCAACACATTTGGGGCCACAGCGCTTCTCAGAG | 360 | | | | | | | |
| Qy | 361 | CTCCAGCTTTGATGGAAGGCTCATGTTGGATGTGGCCACAGGAGGCAAGCTCGAGGCGC | 420 | | | | | | | |
| Db | 361 | CTCCAGCTTTGATGGAAGGCTCATGTTGGATGTGGCCACAGGAGGCAAGCTCGAGGCGC | 420 | | | | | | | |
| Qy | 421 | AGCCATTTGACACCTCACCATCATGCTGTCAGAGCATCCCATGGGTTCCCATAAAGTCA | 480 | | | | | | | |
| Db | 421 | AGCCATTTGACACCTCACCATCATGCTGTCAGAGCATCCCATGGGTTCCCATAAAGTCA | 480 | | | | | | | |
| Qy | 481 | CMCTGCTCTTGGTATCCACGATCGAGGCTGGGGCCAAAGATCTCTTAACATGACGTTAAGCA | 540 | | | | | | | |
| Db | 481 | CMCTGCTCTTGGTATCCACGATCGAGGCTGGGGCCAAAGATCTCTTAACATGACGTTAAGCA | 540 | | | | | | | |
| Qy | 541 | ACGGAAAACCTAAGGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCTTC | 600 | | | | | | | |
| Db | 541 | ACGGAAAACCTAAGGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCTTC | 600 | | | | | | | |
| Qy | 601 | GGCATCATGAANATCGGGGAAGGTCACATACAGATATCTTCAGCTGATGGTATTCG | 660 | | | | | | | |
| Db | 601 | GGCATCATGAANATCGGGGAAGGTCACATACAGATATCTTCAGCTGATGGTATTCG | 660 | | | | | | | |
| Qy | 661 | TTTAAACACGACATCAAAATCCCAAGTCTCTATACTGATGAAGAAGGAGGACGAGAAA | 720 | | | | | | | |
| Db | 661 | TTTAAACACGACATCAAAATCCCAAGTCTCTATACTGATGAAGAAGGAGGACGAGAAA | 720 | | | | | | | |
| Qy | 721 | ACTGATCGGGCAATTTCTGAATTCACATTTTATTCOAATATGTTGGGGGATTTTTCAGC | 780 | | | | | | | |
| Db | 721 | ACTGATCGGGCAATTTCTGAATTCACATTTTATTCOAATATGTTGGGGGATTTTTCAGC | 780 | | | | | | | |
| Qy | 781 | TTCGAGCTGGTGAAGAAATATGACATTCAGGTGTCCAAACCTTCCTCTGCTGATCCGATC | 840 | | | | | | | |
| Db | 781 | TTCGAGCTGGTGAAGAAATATGACATTCAGGTGTCCAAACCTTCCTCTGCTGATCCGATC | 840 | | | | | | | |
| Qy | 841 | AAGATGGACGATCTTTGGGGCTTTCAAAGTTACAGCATAGACTGAGACTCATTTGCTG | 900 | | | | | | | |
| Db | 841 | AAGATGGACGATCTTTGGGGCTTTCAAAGTTACAGCATAGACTGAGACTCATTTGCTG | 900 | | | | | | | |
| Qy | 901 | GAAATATGAGATGATGCTTCTAGATGTTTGGAAACTCTTAAAAAATGATGATGCTAT | 960 | | | | | | | |
| Db | 901 | GAAATATGAGATGATGCTTCTAGATGTTTGGAAACTCTTAAAAAATGATGATGCTAT | 960 | | | | | | | |
| Qy | 961 | ACATGTTTAAGACTACTTAAGAGACATGCCCCAGGTATGAAAACACACAGCCCTCTCTC | 1020 | | | | | | | |
| Db | 961 | ACATGTTTAAGACTACTTAAGAGACATGCCCCAGGTATGAAAACACACAGCCCTCTCTC | 1020 | | | | | | | |
| Qy | 1021 | TTGAGCTGTACAGAGTGTGTATATGTAAAGTCCATAGGTGATGTTGATTCATGGGAT | 1080 | | | | | | | |
| Db | 1021 | TTGAGCTGTACAGAGTGTGTATATGTAAAGTCCATAGGTGATGTTGATTCATGGGAT | 1080 | | | | | | | |

| | | | |
|----|------|---|------|
| QY | 1081 | TACACACGGTTTTACAATTTTGTAAATGATTTCTAGAAATTTGAACCAAGTATGGGAGAGGT | 1140 |
| DB | 1081 | TACACACAGGTTTTACAATTTTGTAAATGATTTCTAGAAATTTGAACCAAGTATGGGAGAGGT | 1140 |
| QY | 1141 | ATTCCGATGCTATGAAGAAACCTACACCTGAGCTATGAGAAAGGGGTACAAGTCTCTGGGT | 1200 |
| DB | 1141 | ATTCCGATGCTATGAAGAAACCTACACCTGAGCTATGAGAAAGGGGTACAAGTCTCTGGGT | 1200 |
| QY | 1201 | CTAACCCCTGGACATGTCGCCACTGAGAACCTTGAATTTAAGAGATGCCATGTCATTGCA | 1260 |
| DB | 1201 | CTAACCCCTGGACATGTCGCCACTGAGAACCTTGAATTTAAGAGATGCCATGTCATTGCA | 1260 |
| QY | 1261 | AAGAAATGATAGTGTGAAGGGTTAAGTCTTTTGAATTTGTAACATTTGGCGTGGGACCGTC | 1320 |
| DB | 1261 | AAGAAATGATAGTGTGAAGGGTTAAGTCTTTTGAATTTGTAACATTTGGCGTGGGACCGTC | 1320 |
| QY | 1321 | AAATAGTTCCTTTTCTTCTAATGAGGAGAGAAAAATATATATTTTATTTATTAATGCTCTA | 1380 |
| DB | 1321 | AAATAGTTCCTTTTCTTCTAATGAGGAGAGAAAAATATATATTTTATTTATTAATGCTCTA | 1380 |
| QY | 1381 | AAATATATTTTCAGGTGTAATGTTTTCTGTGCAAGTTTTGTAAATTAATTTGTGCTAT | 1440 |
| DB | 1381 | AAATATATTTTCAGGTGTAATGTTTTCTGTGCAAGTTTTGTAAATTAATTTGTGCTAT | 1440 |
| QY | 1441 | AGTATTTGATTTAAAAATATTTTAAAAATGTCACAGTGCACATTAATTAATGTTTTAAATG | 1500 |
| DB | 1441 | AGTATTTGATTTAAAAATATTTTAAAAATGTCACAGTGCACATTAATTAATGTTTTAAATG | 1500 |
| QY | 1501 | TACAGATGATTTAACTGCGTGCATTTGTAATTTCCCGTAAGAGTACGTGATGCTAAGGGG | 1560 |
| DB | 1501 | TACAGATGATTTAACTGCGTGCATTTGTAATTTCCCGTAAGAGTACGTGATGCTAAGGGG | 1560 |
| QY | 1561 | GCAGAAATAGTCTTGTGAGACACATGTAATTTCTTATTTCTTTTAACTTAATA | 1620 |
| DB | 1561 | GCAGAAATAGTCTTGTGAGACACATGTAATTTCTTATTTCTTTTAACTTAATA | 1620 |
| QY | 1621 | GAGTCTTCAG | 1630 |
| DB | 1621 | GAGTCTTCAG | 1630 |

[illegible]

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Oy 121 TCTGAGAGATCGCTCTGTTCTCTACTTTCGAGCGCAGATGGATGCTTAACAGATATCAG 180
Dh 121 TCTGAGAGATCGCTCTGTTCTCTACTTTCGAGCGCAGATGGATGCTTAACAGATATCAG 180
Oy 181 AAGACAGACACTGCTGCTTTTATAGAAATCTGAGACTCCATGAAAAAGCAGATTTTGACG 240
Dh 181 AAGACAGACACTGCTGCTTTTATAGAAATCTGAGACTCCATGAAAAAGCAGATTTTGACG 240
Oy 241 ACTGAGCTGAGAGAGTAAAGACACATACCTGACTCCTCGAGAGAGATGAAACAGCCT 300
Dh 241 ACTGAGCTGAGAGAGTAAAGACACATACCTGACTCCTCGAGAGAGATGAAACAGCCT 300
Oy 301 TTCAGGGGGCCGTGAGAGAGAACTGCAACATGTTGGGGCCACAGGCTTCTCAGAG 360
Dh 301 TTCAGGGGGCCGTGAGAGAGAACTGCAACATGTTGGGGCCACAGGCTTCTCAGAG 360
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Dh 481 CTCTGCTCTTGTGATACAGCATGCGAGGCTGGCCAGAGATCTTAACATGACGTTAAACA 540
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Dh 601 GGCATCATGAAACATCGGGAAGCGTACACTACAGATATCTTACGCTGATGCTATGCTCG 660
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Dh 721 ACTGTCGGGGCATTTCTGAATTCACCTTTTATTCATTAATGTTGGGGGATTTTCAAGC 780
Oy 781 TCCGAGCTGGTGAAGAAATTAAGCATTCAGGTGCCAACCCCTTCCCTGCTGATCCGGATC 840
Dh 781 TCCGAGCTGGTGAAGAAATTAAGCATTCAGGTGCCAACCCCTTCCCTGCTGATCCGGATC 840
Oy 841 AAGATGCGACGCTACTTTCGGGCTTTCAAAGTTTCAGAGCATGAGACCTCATTTGCTG 900
Dh 841 AAGATGCGACGCTACTTTCGGGCTTTCAAAGTTTCAGAGCATGAGACCTCATTTGCTG 900
Oy 901 GAACTTTGAGATGATGCTCTAGATGTTTGAACCTTCTTAAAAAATGATGATGCTAT 960
Dh 901 GAACTTTGAGATGATGCTCTAGATGTTTGAACCTTCTTAAAAAATGATGATGCTAT 960
Oy 961 ACATGTGAAGACTACTTAAGAGACATGGCCGAGGTGATGAACCTCAGACCCCTCTC 1020
Dh 961 ACATGTGAAGACTACTTAAGAGACATGGCCGAGGTGATGAACCTCAGACCCCTCTC 1020
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Oy 1261 AAGAAATGATAGTGAAGGCTTAAGTCTTTTGAATTTGATACATTTGGCTGGGACCTGTC 1320
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Dh 1321 AAATTAAGTCTTTTCTTTTCTTAATGAGAGAGAAATATATGATATTTTATTAATGCTCA 1380
Oy 1381 AAGTATATTTACAGGTGAATGTTTCTGCAAGATTTTGTAAATATATTTGGCTAT 1440
Dh 1381 AAGTATATTTACAGGTGAATGTTTCTGCTCAAGATTTTGTAAATATATTTGGCTAT 1440
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Dh 1441 AGTATTTGATTCAAATATTTTAAAAATGCTCACGTGTTGACATATTTAAATGTTTAAATG 1500
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Oy 1621 GAGTCTTCAG 1630
Dh 1621 GAGTCTTCAG 1630

RESULT 3
AX147987
LOCUS AX147987 1630 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 10 from Patent WO0136637.
ACCESSION AX147987
VERSION AX147987.1 GI:14346962
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1630)
AUTHORS Anderson,D.M. and Hughes,A.E.
TITLE Receptor activator of nf-kappa b
JOURNAL Patent: WO 0136637-A 10 25-MAY-2001;
Immunex Corporation (US)
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BASE COUNT 436 a 355 c 379 g 460 t
ORIGIN

Query Match 100.0%; Score 1630; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| OY | 1 | CCGGCGTCCACACGAGGGTCCGCTGACACCCCGGCCCTTTCTGCACGGGCTCCGGCGCCG | 60 |
| Db | 1 | CCGGCGTCCACACGAGGGTCCGCTGACACCCCGGCCCTTTCTGCACCGGCTCCGGCGCCG | 60 |
| OY | 61 | CACCGCGCGCTCCCGCCTCCATGTTCTGCGCCCTCTGGGGCTGGGACTGGGCGAGGTG | 120 |
| Db | 61 | CACCGCGCGCTCCCGCTCCATGTTCTGCGCCCTCTGGGGCTGGGACTGGGCGAGGTG | 120 |
| OY | 121 | TCGCGACGATCGCTCTGTTCTCTGTACTTTCCAGCGCGACATGATGATCTTAACGAATATCAG | 180 |
| Db | 121 | TCGCGACGATCGCTCTGTTCTCTGTACTTTCCAGCGCGACATGATGATCTTAACGAATATCAG | 180 |
| OY | 181 | AAGACGACGATCTACTGCTTTTATAGATCTCTAGACTCTCATGAAACGACAGATTTCGAG | 240 |
| Db | 181 | AAGACGACGATCTACTGCTTTTATAGATCTCTAGACTCTCATGAAACGACAGATTTCGAG | 240 |
| OY | 241 | ACTGCACTGTGAGAGTGAAGACACACTACTGACTCTGTGAGAGAGATGAACAGACTT | 300 |
| Db | 241 | ACTGCACTGTGAGAGTGAAGAGACACTACTGACTCTGTGAGAGAGATGAACAGACTT | 300 |
| OY | 301 | TTTCAGGGGGCGCGTGCAGGAAGAACTGCAACATATGTGGGGCGACAGGCTTCCAGAG | 360 |
| Db | 301 | TTTCAGGGGGCGCGTGCAGGAAGAACTGCAACATATGTGGGGCGACAGGCTTCCAGAG | 360 |
| OY | 361 | CTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCAGCGAGGCAAGCCTGAGGCC | 420 |
| Db | 361 | CTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCAGCGAGGCAAGCCTGAGGCC | 420 |
| OY | 421 | AGCCATTGTCACACCTCCACATCAATGACGCGCCAGATCCATCGGGCTCCCATTAATCA | 480 |
| Db | 421 | AGCCATTGTCACACCTCCACATCAATGACGCGCCAGATCCATCGGGCTCCCATTAAGCA | 480 |
| OY | 481 | CTCTGCTCTTGTGTACACGATCGAGGCTGGGGCCAAAGTCTTAACATGACGTTAAGCA | 540 |
| Db | 481 | CTCTGCTCTTGTGTACACGATCGAGGCTGGGGCCAAAGTCTTAACATGACGTTAAGCA | 540 |
| OY | 541 | ACGNAAACTAAGGTTAAACCAAGATGGCTTCTATTACTGTACCCCAACATTTGCTTC | 600 |
| Db | 541 | ACGNAAACTAAGGTTAAACCAAGATGGCTTCTATTACTGTACCCCAACATTTGCTTC | 600 |
| OY | 601 | GGCATTCATGAACACTCGGGAAGGCTACTACAGACTATCTTCAGGTGATGTATGCG | 660 |
| Db | 601 | GGCATTCATGAACACTCGGGAAGGTAACCTAACAGACTATCTTCAGGTGATGTATGCG | 660 |
| OY | 661 | TTAAACACGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGACACGAAA | 720 |
| Db | 661 | TTAAACACGAGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGGAGGACGAAA | 720 |
| OY | 721 | ACTGCTGGGGCAATTCGAATTCACCTTTATTCCTAATAATTTGGGGATTTTTCAAAG | 780 |
| Db | 721 | ACTGCTGGGGCAATTCGAATTTCCACTTTTATTCCTAATAATTTGGGGATTTTTCAAAG | 780 |
| OY | 781 | TCCGAGTGGTGAAGAAATTAGCATTCAGGTGCCAACCCCTCCCTGCTGATCCGAGTC | 840 |
| Db | 781 | TCCGAGTGGTGAAGAAATTAGCATTCAGGTGCCAACCCCTCCCTGCTGATCCGAGTC | 840 |
| OY | 841 | AAGATGCGAGCTACTTTGGGGCTTTCAAAGTTCCAGACATTAACGACGATCATTTGCTG | 900 |
| Db | 841 | AAGATGCGAGCTACTTTGGGGCTTTCAAATTCAGACATTAACGACGATCATATTGCTG | 900 |
| OY | 901 | GAACATTAGCATGATGATGCTCTAGATGTTTGGAAACTCTTAAATAAATGATGATGCTAT | 960 |
| Db | 901 | GAACATTAGCATGATGATGCTCTAGATGTTTGGAAACTCTTAAATAAATGATGATGCTAT | 960 |
| OY | 961 | ACATGTGTAGACTACTAAGAGACATGCCCCAGGTGTATGAAACTCACAGCCCTCTCTC | 1020 |
| Db | 961 | ACATGTGTAAAGACTACTAAGAGACATGCCCCAGGTGTATGAAACTCACAGCCCTCTCTC | 1020 |
| OY | 1021 | TTGAGCCGTACAGGTGTGTATATATGAAGATCCATAGGTGATGTTAGATTATGATGAT | 1080 |
| Db | 1021 | TTGAGCCGTGTACAGGTGTGTATATATGAAGATCCATAGGTGATGTTAGATTATGATGAT | 1080 |
| OY | 1081 | TACACACGGTTTTTACAATTTTGTATAGATTTCTTGAAATTAACACAGATTGGAGAGGT | 1140 |

| Db | 1081 | TACACACAGTTTATACATTTTGTATGATTTTCCATGAAATTTGAACACATTTGGAGAGT | 1140 |
|-----------|------------|--|------|
| Qy | 1141 | ATTCGATGCTTATGAAGAACTTACAGCTAGCTATGSAAGGGGTCCAGTCTGGGT | 1200 |
| Db | 1141 | ATTCGAGCTTATGAAGAACTTACACGTGAGCTATGGAAGGGGTCCAGTCTGGGT | 1200 |
| Qy | 1201 | CTAACCCCTGGACATGTGCCACTGAGACCTTGAATTAAGATGTCATGTAATGCA | 1260 |
| Db | 1201 | CTAACCCCTGGACATGTGCCACTGAGAACCTTGAATTAAGATGTCATGTAATGCA | 1260 |
| Qy | 1261 | AAGAAATGATAGTGTGAAGGCTTAAGCTTTTGAATTTGTTACATTCGCTGGACCTGC | 1320 |
| Db | 1261 | AAGAAATGATAGTGTGAAGGCTTAAGCTTTTGAATTTGTTACATTCGCTGGACCTGC | 1320 |
| Qy | 1321 | AAATAGTCTTTTCTTTCTATATGAGGAGAGAAAATATGATTTTATATATATGCTTA | 1380 |
| Db | 1321 | AAATAGTCTTTTCTTTCTATATGAGGAGAGAAAATATGATTTTATATATATGCTTA | 1380 |
| Qy | 1381 | AAGTAAATTTTCAGGTGTAAATGTTTTTCGTGCAAGTTTGTAAATTAATTTGTCTAT | 1440 |
| Db | 1381 | AAGTAAATTTTCAGGTGTAAATGTTTTTCGTGCAAGTTTGTAAATTAATTTGTCTAT | 1440 |
| Qy | 1441 | AGTATTTGATTCAAATATTTTAAAAATGCTCAGCTGTGACATATTAATGTTTAAATG | 1500 |
| Db | 1441 | AGTATTTGATTCAAATATTTTAAAAATGCTCAGCTGTGACATATTAATGTTTAAATG | 1500 |
| Qy | 1501 | TACAGATGATTTTAACTGATGTCACCTTTTAAATTCCTCCGAAAGTACTGATGCTAAGGG | 1560 |
| Db | 1501 | TACAGATGATTTTAACTGATGTCACCTTTTAAATTCCTCCGAAAGTACTGATGCTAAGGG | 1560 |
| Qy | 1561 | GCAGAAATACGTGTTCTGGTGACACATGATGTTTATCTTATCTTTTAACATAA | 1620 |
| Db | 1561 | GCAGAAATACGTGTTCTGGTGACACATGATGTTTATCTTATCTTTTAACATAA | 1620 |
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| Db | 1621 | GAGTCTTCAG 1630 | |
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| LOCUS | DEFINITION | Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, complete cds. | |
| ACCESSION | AF019048 | | |
| VERSION | AF019048.1 | GI:2612923 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| MEDLINE | | | |
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| AUTHORS | | | |
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BASE COUNT 623 a 468 c 523 g 611 t
ORIGIN

Query Match 100.0%; Score 1630; DB 10; Length 2225;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
AR062119
LOCUS AR062119 2295 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5843678.
ACCESSION AR062119
VERSION AR062119.1 GI:5989810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle,W.J.

TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1. 2295
BASE COUNT 648 a 487 c 538 g 622 t
ORIGIN

Query Match 99.9%; Score 1628.4; DB 6; Length 2295;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 282 CACCCGCGCCCTCCCGCTCCATGTTCTGCGCCCTCTGCGGCTGGGACTGGGCGCAGGTGG 341
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OY 1621 GAGTCTTCAG 1630
DB 1842 GAGTCTTCAG 1851
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RESULT 6
AF053713 2299 bp mRNA linear ROD 09-MAY-1998
LOCUS AF053713
DEFINITION Mus musculus osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053713
VERSION AF053713.1 GI:3057147
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2299)
Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Caparrelli, C., Eli, A.,
Dian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J., and Boyle, W.-J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
Cell 93 (2), 165-176 (1998)

MEDLINE 98227661
REFERENCE 2 (bases 1 to 2299)
AUTHORS Boyle, M. J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA

FEATURES

Source Location/Qualifiers
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ICFRHETSGSVPTDYQLMAYVYKTSIKIPSSHLKMGSTKMSNSEHFYSINV
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BASE COUNT 641 a 494 c 541 g 623 t
ORIGIN

Query Match 99.9% Score 1628.4; DB 10; Length 2299;
Best Local Similarity 99.9% Pred. No. 0;

Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| VERSION | ARI57058.1 | GI:15125762 | | | |
| KEYWORDS | . | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | Unclassified. | | | | |
| AUTHORS | 1 (bases 1 to 2191) | | | | |
| TITLE | Gorman,D.M. and Mattson,J.D. | | | | |
| JOURNAL | Mammalian cell surface antigens: related reagents | | | | |
| FEATURES | Patent: US 6242586-A 1 05-JUN-2001; | | | | |
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| OY | 121 | TCCTGACAGATCGCTCTGTTCTGTGTACTTTC | GTGAGCCGATGATGGATCTTAACAGAAATTCAG | 180 |
| Db | 309 | TCCTGACAGATCGCTCTGTTCTGTGTACTTTC | GTGAGCCGATGATGGATCTTAACAGAAATTCAG | 368 |
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| Db | 429 | ACTGCACTCTGAGAGTGAAGACACACTACCTG | ACTCTGTCAGAGAGATGAACAAGACCT | 488 |
| OY | 301 | TTTCAGGGGGCCGTGCAGAAAGAACTGCACAC | ATTGTGGGGCCACAGCGCTTCTCAGGAG | 360 |
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| Qy | 841 | AAGATGCCAGTACTTTGGGGCTTTCAAAGTTCAGAGCATATAGACTGAGACATTTGGTG | 900 |
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| SOURCE | unidentified. | | | |
| ORGANISM | unidentified | | | |
| | unclassified. | | | |

REFERENCE 1 (bases 1 to 2191)
AUTHORS Gorman,D.M. and Maltson,J.D.
TITLE Mammalian cell surface antigens, related reagents
JOURNAL Patent: EP 114864-A 1 11-JUL-2001;
SCHERING CORPORATION (US)
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AF013170 AF013170 2237 bp mRNA linear ROD 05-NOV-1998
LOCUS DEFINITION Mus musculus TNF-related ligand TRANCE mRNA, complete cds.
ACCESSION AF013170

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VERSION      AF013170.1  GI:2411497
KEYWORDS
SOURCE       house mouse.
ORGANISM     Mus musculus.
REFERENCE    Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 2237)
              Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlickick,J., Chao,M.,
              Kalchikov,S., Cayan,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
              and Choi,Y.
TITLE        TRANCE is a novel ligand of the tumor necrosis factor receptor
JOURNAL      J. Biol. Chem. 272 (40), 25190-25194 (1997)
MEDLINE      97460112
REFERENCE    2 (bases 1 to 2237)
AUTHORS      Wong,B.R., Josien,R., Lee,S.Y., Sauter,B., Li,H.L., Steinman,R.M.
              and Choi,Y.
TITLE        TRANCE (tumor necrosis factor [TNF]-related activation-induced
JOURNAL      cytoline), a new TNF family member predominantly expressed in T
MEDLINE      cells, is a dendritic cell-specific survival factor
REFERENCE    J. Exp. Med. 186 (12), 2075-2080 (1997)
AUTHORS      3 (bases 1 to 2237)
              Fuller,K., Wong,B., Fox,S., Choi,Y. and Chambers,T.J.
TITLE        TRANCE is necessary and sufficient for osteoclast-mediated
JOURNAL      activation of bone resorption in osteoclasts
MEDLINE      J. Exp. Med. 188 (5), 997-1001 (1998)
REFERENCE    4 (bases 1 to 2237)
AUTHORS      Choi,Y., Josien,R., Lee,S.Y., Volododskala,M., Steinman,R.M. and
              Chol,Y.
TITLE        The TRAF family of signal transducers mediates NF-kappaB activation
JOURNAL      by the TRANCE receptor
MEDLINE      J. Biol. Chem. 273 (43), 28355-28359 (1998)
REFERENCE    5 (bases 1 to 2237)
AUTHORS      Mong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
TITLE        Direct Submission
JOURNAL      Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
MEDLINE      Rockefeller University, 1230 York Ave., New York, NY 10021, USA
REFERENCE    Location/Qualifiers
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RESULT 10

E34349

LOCUS E34349 2029 bp DNA linear PAT 31-JAN-2002

DEFINITION DNA and process for producing protein by using the same.

ACCESSION E34349.1 GI:18624334

VERSION JP 2000102390-A/4.

KEYWORDS

SOURCE

ORGANISM

Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 2029)

Mizuno, A., Kodaira, K. and Kodaira, Y.

DNA and process for producing protein by using the same

Patent: JP 2000102390-A 4 11-Apr-2000;

SNOW BRAND MILK PROD CO LTD, YS NEW TECHNOLOGY LAB

OS Mus sp. (mouse)

PN JP 2000102390-A/4

PD 11-APR-2000

PR 30-SEP-1998 JP 1998292971

PI

ATSUKO MIZUNO, KUNIHICO KODAIRA, YASUKO KODAIRA PC

C12N15/09, A61K31/00, C07K14/47, C12P21/02, C12Q1/68, (C12N15/09, PC

C12R1:91),

PC (C12P21/02, C12R1:91), C12N15/00, (C12N15/00, C12R1:91) CC

FH

Key Location/Qualifiers

FT CDS (159)..(380).

FEATURES

source

1..2029 Location/Qualifiers

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DEFINITION complete cds.
ACCESSION AB022039
VERSION AB022039.1 GI:4127268
KEYWORDS osteoclast differentiation factor.
SEGMENT 4 of 4
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Kodaira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N.,
Murakami,A., Ueda,M. and Higashio,K.
TITLE Cloning and characterization of the gene encoding mouse osteoclast
differentiation factor
JOURNAL Gene 230 (1), 121-127 (1999)
MEDLINE 99214075
REFERENCE 2 (bases 1 to 2029)
AUTHORS Kodaira,K.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1999) Kunihiko Kodaira, Chugai Pharmaceutical
Co., LTD.; 301 Fujii, 6-19 Nakamachi, Hannou-city, Saitama 357-0038,
Japan (E-mail:kodaira@kai.or.jp; Tel:81-33987-0594)
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AF053712

LOCUS AF053712 2271 bp mRNA linear PRI 09-MAY-1998
DEFINITION Homo sapiens osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053712
VERSION AF053712.1 GI:3057145
KEYWORDS
SOURCE
ORGANISM human.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Olan, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J. and Boyle, W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle, W.J.
TITLE Direct Submision
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
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| DEFINITION | | (RANKL) mRNA, complete cds. | | |
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| AUTHORS | | 1 (bases 1 to 2201) | | |
| | | Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C., | | |
| | | Tometsko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and | | |
| | | Galibert,L. | | |
| TITLE | | A homologue of the TNF receptor and its ligand enhance T-cell | | |
| JOURNAL | | growth and dendritic-cell function | | |
| MEDLINE | | Nature 390 (6656), 175-179 (1997) | | |
| REFERENCE | | 98032977 | | |
| AUTHORS | | 2 (bases 1 to 2201) | | |
| | | Cosman,D.M., Billingsley,W., Dougall,W., Maraskovsky,E., | | |
| TITLE | | Anderson,D., Dubose,R. and Galibert,L. | | |
| JOURNAL | | Direct Submission | | |
| | | Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51 | | |
| | | University St., Seattle, WA 98101, USA | | |
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E34350 951 bp DNA linear PAT 31-JAN-2002

LOCUS E34350 DNA and process for producing protein by using the same.

DEFINITION E34350

ACCESSION E34350.1 GI:18624335

VERSION E34350.1

KEYWORDS JP 2000102390-A/5.

SOURCE Mus sp.

ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 951)

AUTHORS Mizuno,A., Kodaira,K. and Kodaira,Y.

TITLE DNA and process for producing protein by using the same

JOURNAL Patent: JP 2000102390-A 5 11-APR-2000;

SNOW BRAND MILK PROD CO LTD,YS NEW TECHNOLOGY LAB

COMMENT OS Mus sp. (mouse)

PN JP 2000102390-A/5

PD 11-APR-2000

PF 30-SEP-1998 JP 1998292971

PR

PI ATSUOKO MIZUNO, KUNIHICO KODAIRA, YASUOKO KODAIRA, PC

C12N15/09,A61K31/00,C07K14/47,C12P21/02,C12Q1/68//C12N15/09, PC

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FT Location/Qualifiers

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Qy 841 AAGATCGGAGTACTTGGGCTTCAAGAGTTCAGGACATAGACTGA 887

Db 905 AAGATCGGAGTACTTGGGCTTCAAGAGTTCAGGACATAGACTGA 951

RESULT 15

E36388 951 bp DNA linear PAT 07-FEB-2001

LOCUS E36388 Novel protein, DNA and utilization thereof.

DEFINITION E36388

ACCESSION E36388.1 GI:13017477

VERSION

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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(without alignments)
6857.057 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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| 15 | 885.4 | 54.3 | 951 | 21 | AA39156 | Mouse OBM nucleoti |
| 16 | 885.4 | 54.3 | 951 | 21 | AA299365 | DNA encoding a mur |
| 17 | 885.4 | 54.3 | 951 | 21 | AA299365 | Osteoclast formati |
| 18 | 832.8 | 51.1 | 1823 | 20 | AAV80223 | Human TRANCE encod |
| 19 | 773.4 | 47.4 | 957 | 22 | AAV86481 | Rat osteoclast dif |
| 20 | 764.6 | 46.9 | 1574 | 22 | AAH25526 | Nucleotide sequenc |
| 21 | 733.4 | 45.0 | 735 | 19 | AAV69898 | Nucleic acid encod |
| 22 | 615 | 37.7 | 954 | 19 | AAV41378 | NF-kB receptor act |
| 23 | 615 | 37.7 | 954 | 19 | AAV41372 | NF-kB receptor act |
| 24 | 615 | 37.7 | 954 | 22 | AAV41311 | Human receptor act |
| 25 | 615 | 37.7 | 954 | 22 | AAV41311 | Human receptor act |
| 26 | 615 | 37.7 | 954 | 22 | AAV41311 | Human receptor act |
| 27 | 611.8 | 37.5 | 954 | 22 | AAV41311 | Human receptor act |
| 28 | 520.6 | 31.9 | 741 | 19 | AAV69899 | Human full-length |
| 29 | 466 | 28.6 | 522 | 22 | AAV69899 | Nucleic acid encod |
| 30 | 313.2 | 19.2 | 564 | 21 | AAV13369 | Mouse cDNA encodin |
| 31 | 312.2 | 19.2 | 519 | 21 | AA299368 | DNA encoding a syn |
| 32 | 312.2 | 19.2 | 519 | 21 | AA299369 | DNA encoding a syn |
| 33 | 278.6 | 17.1 | 519 | 21 | AA299372 | DNA encoding a mur |
| 34 | 262.4 | 16.1 | 519 | 21 | AA299371 | DNA encoding osteo |
| 35 | 259.4 | 15.9 | 519 | 21 | AA299373 | DNA encoding osteo |
| 36 | 247.6 | 15.2 | 564 | 21 | AA299370 | DNA encoding osteo |
| 37 | 165.8 | 10.2 | 468 | 21 | AAV39153 | Mouse OBM nucleoti |
| 38 | 157.8 | 9.7 | 2026 | 21 | AAV39152 | Mouse OBM nucleoti |
| 39 | 120.6 | 7.4 | 254 | 20 | AAV56001 | Human Tumour necro |
| 40 | 105.8 | 6.5 | 575 | 21 | AAV39154 | Mouse OBM nucleoti |
| 41 | 58.4 | 3.6 | 656 | 21 | AAV38005 | Cell factor deriva |
| 42 | 58.4 | 3.6 | 759 | 22 | AAV18398 | GH-derived leader |
| 43 | 58.4 | 3.6 | 768 | 22 | AAV18399 | CMV-derived leader |
| 44 | 58.4 | 3.6 | 801 | 22 | AAV03112 | Ompa signal peptid |
| 45 | 58.4 | 3.6 | 846 | 19 | AAV42205 | TNF-related apopto |

ALIGNMENTS

| | | |
|----------|---|--|
| RESULT 1 | | |
| ID | AAV41377 | standard; cDNA; 1630 BP. |
| AC | AAV41377: | |
| XX | | |
| AC | | |
| XX | | |
| DT | 08-OCT-1998 | (first entry) |
| XX | | |
| DE | NF-kB receptor activator RANK ligand (RANKL) encoding cDNA. | |
| XX | | |
| KW | RANK: necrosis factor-kappa B; NF-kB: receptor activator; human | |
| KW | immune response; inflammatory response; toxic shock; sepsis; | |
| KW | RANKL: RANK ligand; tumour necrosis factor; TNF; mouse; ss. | |
| OS | Mus musculus. | |
| XX | | |
| FH | | |
| FT | Key | Location/Qualifiers |
| FT | CDS | 3..887 |
| FT | | /*tag= a |
| FT | | /product= "murine RANKL (ligand for RANK)" |
| XX | | |
| PN | W09828426-A2. | |
| XX | | |
| PD | 02-JUL-1998. | |
| XX | | |
| PF | 22-DEC-1997; | 97WO-US23775. |
| XX | | |
| PR | 14-OCT-1997; | 97US-0064671. |
| PR | 23-DEC-1996; | 96US-0059978. |
| PR | 07-MAR-1997; | 97US-0813509. |
| XX | | |
| PA | (IMMV) IMMUNEX CORP. | |

XX PI Anderson DM, Galibert LJ, Maraskovsky E;
XX PI WPI: 1998-377657/32.
DR P-PSDB; AAM69956.
XX
PT New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells
XX
PS Claim 25; Pages 55-57; 80pp; English.
XX
CC This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappab (NF-kB)) polypeptide. RANK is a
CC member of the tumor necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g., in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.
XX
SQ Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;
Query Match 100.0%; Score 1630; DB 19; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCGGGCTCCACAGAGGGTCCGCTGACACCCGGGCTTCGACACCGGCTCCGGGGCCG 60
DB 1 ccgggctccacagaggggtccgctgacacccgggcttcgacacccgggtccggggccg 60
OY 61 CACCGCGCCGCCGCCGCTCATGATCTCTGCGCCCTCTGGGCTGGAGTGGGCCAGTGG 120
DB 61 caccgcgccgccgccgctcatgatctctgcgccctctgggctggagtgggccagtg 120
OY 121 TCTGCAGCATGCGTCTGTCTCTGTTCTTCTGACGCGAGATGGATCTTACAGAAATATCAG 180
DB 121 tctgcagcatgctgtctgtctctgttctctgactctcgagcgagatgattctacaagaatatacag 180
OY 181 AAGACAGACATCTACGCTTTTATAGATCTGAGACTCCATGAAACGAGATTGGCAGG 240
DB 181 aagaacagacatctacgcttttatagactctgagactccatgaagaacgagattggcagg 240
OY 241 ACTGCAGCTGGAGAGTGAAGACACACTACTGACTCTCTGACGAGAGATGAAACAGCCT 300
DB 241 actgcagctggagagtgaaagacacactactgactctctgacgagagatgaaacagcct 300
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DB 301 ttcagggggcgctgcagaaagaaactgcaaacacttgtggggccacagcgcttctgagag 360
OY 361 CTCACGCTATGATGGAAGGCTCATGTTGATGTGGCCAGGAGGAGGAGCTTGAGAGCC 420
DB 361 ctcacgctatgatggaaggctcatgtttgatgtggccaggagaggagcttgagagcc 420
OY 421 AGCATTGTCACACCTCACATCAATGCTGCGACGATCCCATCGGGTCCATAAGTCA 480
DB 421 agcattgtcacacctcacatcaatgctgcgacgattcccatcggggtccataagtca 480
OY 481 CTCGTCTCTCTTGTGTACCAAGATGAGGCTGGGCAAGATCTCTTAACATGAGCTTAAGA 540

DB 481 ctcgtctctcttgtgtacccaagatcgaggtgagccaaagctctacaagatgaaga 540
OY 541 ACGGAATACTAAGGGTTACCAAGATGCGTCTTATTAACCTGACGCAACATTTGTTTC 600
DB 541 acggaataactaagggttaaccaagatgctcttatacttaacgtcaagcacaattgcttc 600
OY 601 GGCATCATGAACATCGGAGAGGCTACTACAGACTATCTTCAGCTGATGTATGTGC 660
DB 601 ggcatacatgaacatcggaaggctactacagactatcttcagctgagtgtatgtcg 660
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DB 661 ttaaacacagcatcaaaatcccaagttctcataacctga tgaagagagagcaaga 720
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DB 721 acagtcgggcaattcctgattccttacttacttcaataatgttggggattttcaac 780
OY 781 TCCGAGCTGTGAAGAAATTAGCATTCAGGTGTCAACCTTCCTGCTGGATCCGATC 840
DB 781 tcgagctgtgaaagaattagatgattccaggtgtccaaccttcctcgtgaltccgaltc 840
OY 841 AAGATCGACGTACTTTGGGGCTTTCAAAGTTGAGACATAGACTGAGCTCATTTCTGTC 900
DB 841 aagatcgacgtactttggggctttcaaagttgagacatagactgagctcatTTCTGTC 900
OY 901 GAACATTCAGATGATGCTCTAGATGTTTGGAACCTCTTAAATAATGATGATGTCTAT 960
DB 901 gaacattagatgatgctctagatgtttggaacctcttAAATAATGATGATGTCTAT 960
OY 961 ACATGTGTAAGACTACTTAAGAGACATGCGCCAGGCTGTATGAACACACGCGCTCTGC 1020
DB 961 acatgtgtgaagactacttaagagacatgcgccaggctgtatgaacacacgctctgc 1020
OY 1021 TTGAGCCTGTACAGCTGTGTGATGTATGTAAGTCAATGATGATGATTCATGATGAT 1080
DB 1021 ttgagcctgtacagctgtgtgattgtatgtaagtcattgtaagtcattgtaagtcattg 1080
OY 1081 TACACAACGGTTTTACATTTTGTATGATTTCTTACATTTGAACCGATTTGGAGAGGT 1140
DB 1081 tacacaacggTTTTACATTTTGTATGATTTCTTACATTTGAACCGATTTGGAGAGGT 1140
OY 1141 ATTCCGATGCTTATGAATAAATTACAGTGTGAGTGAAGGGGCTACAGTCTCTGGT 1200
DB 1141 attccgatgcttTATGAATAAATTACAGTGTGAGTGAAGGGGCTACAGTCTCTGGT 1200
OY 1201 CTAACCCCTGGACATGTGCGCACTGAGAACCTTGAAATTTAAGAGATGCCATGTCTTGA 1260
DB 1201 ctaacccctggacatgtgCGCACTGAGAACCTTGAAATTTAAGAGATGCCATGTCTTGA 1260
OY 1261 AAGAAATGATAGTGTGAAGGTTTAAGTTCTTTGAAATTTGATACATTCGCGGAGACCTGC 1320
DB 1261 aagaatgatagtggtgaaggtttaagttctttgaaatTTGATACATTCGCGGAGACCTGC 1320
OY 1321 AAATTAAGTTCTTTTCTTAATGAGAGAGAAATAATATGATTTATTTATTTATGTCCTA 1380
DB 1321 aaatTAAGTTCTTTTCTTAATGAGAGAGAAATAATATGATTTATTTATTTATGTCCTA 1380
OY 1381 AAGTTATTTTCAGGTGTAATGTTTCTGTGCAAGTTTGTAAATTAATTTATTTGTGCTAT 1440
DB 1381 aagttatTTTCAGGTGTAATGTTTCTGTGCAAGTTTGTAAATTAATTTATTTGTGCTAT 1440
OY 1441 AGTATTTGATTCAAAATTTTAAATAATCTTCACAGTTGAGATTTTAAATGTTTAAATG 1500
DB 1441 agtatttGATTCAAAATTTTAAATAATCTTCACAGTTGAGATTTTAAATGTTTAAATG 1500
OY 1501 TACAGATGATTTAATCTGGTGCATTTTAAATTCCTCTGAAGAGTACTGTAGCTAAGGGG 1560
DB 1501 tacagatgattTAAATCTGGTGCATTTTAAATTCCTCTGAAGAGTACTGTAGCTAAGGGG 1560
OY 1561 GCAGATAACTGTTTCTGTGACACATGATGATTTATTTCTTTATTTTAACTTAATA 1620

Db 1561 gcagatactcttcgtgacacacatgtagttattcttcttacttcttaacttaata 1620
QY 1621 GAGTCTTCAG 1630
 |||||
Db 1621 gactcttcag 1630

RESULT 2
AAV41371
ID AAV41371 standard; cDNA; 1630 BP.
XX
AC AAV41371;
XX
DT 08-OCT-1998 (first entry)
XX
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 3..887
FT /*tag= a
FT /product= "murine RANKL (ligand for RANK)"
XX
PN M00828424-A2.
XX
PD 02-JUL-1998.
XX
PE 22-DEC-1997; 97WO-0523866.
XX
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
PA (IMMEX) IMMUNEX CORP.
XX
PI Anderson DM, Gallbert LJ, Maraskovsky E;
XX
DR WPI: 1998-377655/32.
DR P-PSDB: AAM68292.
XX
PT New isolated receptor activator of necrosis factor-kappa B - useful
PT for, e.g. developing products for regulating an immune or
PT inflammatory response, treating toxic shock or sepsis
XX
PS Example 7; Pages 55-57; 80pp; English.
XX
CC This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. Host cells transformed
CC or transfected with an expression vector comprising the RANK encoding
CC nucleic acid can be used to produce recombinant RANK protein. The soluble
CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC used for regulating an immune or inflammatory response. Inhibition of
CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
CC of an inflammatory response that result from triggering of RANK, e.g. in
CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC inflammatory reactions. They can also be used in adjunct therapy for
CC disease characterised by neoplastic cells that express RANK. The products
CC can also be used for detection and drug screening.
XX
SO Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Query Match 100.0%; Score 1630; DB 19; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGCGTCCACACGAGGGTCCGTCGACCCCGCCCTTCTGACCGGCTCCGGCGCC 60
 |||||
Db 1 ccggcggtcccaacagaggtcgtcgctgacccccgctctcgaccggtctccggcgcc 60
QY 61 CACCCGCCGCTCCCGCTCCATGTTCTCGGCGCTTCGGGCGTGGGCGCCAGGTGG 120
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Db 61 caccgcgcctcccgctccatcagcttcctgccccctcggcctggagcgtggccaggtgg 120
QY 121 TTCTGACGATGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 |||||
Db 121 tctgagacatcgctcgtctcctgtaacttcgagcgcagatggaatccaaagaaatcag 180
QY 181 AAGACAGCACTCACTGCTTTTATAGAAATCCGAGACTTCATGAAAGCAGATTGCGAG 240
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Db 181 aagacagacactcaactgcttttatagaatcctggaactccatgaaacgcgatttcagg 240
QY 241 ACTGCACTCTGAGAGTGAAGACACACTACCTGACTCTCGAGAGAGATGAAMACGCT 300
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Db 241 actgactctgagagatggaagacacactacactgactctcctcgagaggaatgaaacagcct 300
QY 301 TTTCAGGGGCGCTGTCAGAGAACTGCAACACATTTGGGGCCACAGCGTTCTCAGAG 360
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Db 301 ttccaggggcccgtgcagaggaactgcaacacatctgaggccacagcgtctccaggag 360
QY 361 CTCGAGCTATGATGGAAGGCTCATGTTGATGCGCCGACGCGCAAGCGCTGAGCGCC 420
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Db 361 ctccagctatgagatggaaggtcctcgtgtgagtcgcccagcgaagcctcgaagccc 420
QY 421 AGCCATTGGCACACCTCAGCATCAATGCTGCGACATCCATCGGTTCCCATTAAGTCA 480
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Db 421 agccattgcaacactcaacacatcaatgctgcagacatcccatcggtctccatgaagtc 480
QY 481 CTCGTCTCTGTGTGTACAGATGAGGCTGGGCAAGATCTCTAATGACGTTAAGCA 540
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Db 481 ctctgtctctctgtgtacacagatcgaaggtcgggcaagacatccaaatgacgtlaagca 540
QY 541 ACGGAACATAAGGCTTAACCAAGATGGCTTCTATTACTGTACGCAACATTTGCTTTC 600
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Db 541 acggaacataaggtttaaccaaagatgctctctctatccgtgaagccaaatctgtcttc 600
QY 601 GGCATCATGAACATCGGGAAGCTACCTACAGATCTTTCAGCTGATGCTGATGCTG 660
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Db 601 ggcatactgaacatcgggaagcgtacctacagactctctcagctgagtgtatgcg 660
QY 661 TTAAACACGATCAATAATCCAAAGTCTCATTAACGATGAAGGAGGAGACAGCAAAA 720
 |||||
Db 661 ttaaacacgatacaataatcccaagttctcataaacctcgatgaaggaagacagaaa 720
QY 721 ACTGCTGGGCAATTCTGAATTCACATTTTATTCATTAATGTTGGGGAATTTTCAAGC 780
 |||||
Db 721 actgctgggcaattctgaaatctcaactcttaactcaataatgltggggatcttccaagc 780
QY 781 TCCGAGCTGCTGAAGAAATTAAGATTAAGCTGTCAACCTTCCCTGCTGATCCGATC 840
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Db 781 tccgagctgtgtgaagaatattgcatcagggtgtccaaacctctcctgtgaccgagatc 840
QY 841 AAGATCGGAGCTACTTGGGGCTTTCAAGATTCAGAGCATGAGCTGACTATTCGTG 900
 |||||
Db 841 aagatcggaagctacttgggggtcttcaaaatcagagcaatagactcagactcctcg 900
QY 901 GAACATTAGCATGGAGTCTCTAGATGTTTGAAGAACTTTTAAAGATGATGATGCTAT 960
 |||||
Db 901 gaacattagcatgagatgctctagatgtgttgaaactcttcaaaaatggtgtgtctat 960
QY 961 ACATGTGTAGACTACTTAAGAGACATGGCCACGAGGTATGAACATCACAGCCTCTCTC 1020
 |||||
Db 961 acatgtgttagactacttaagaagacatgcccacggtgtatgaaactcaagccctctctc 1020
QY 1021 TTGAGCCTGTACAGGTTGTATATATGTAAGTCCATGAGTGAATGATTAAGTTCAGTAT 1080
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Db 1021 ttgagcctgtacaggtgtgtatataatgtaagtcacataggtgagatgatcatcgtgat 1080

| | | | |
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| Oy | 1081 | TACAAAGCGTTTTCACAATTTTGTAATGATTTCCTGGAAFTTGAACCAAGATTGGAGAGGT | 1140 |
| Db | 1081 | tacaaagcglltttccaatttcgtlaatgatlccctagaattgaaccagatcgggaagglt | 1140 |
| Oy | 1141 | ATTCCGATCCTTATGCAGAAAACCTTACACGAGAGCTATGAGAAGGGGGTCACAGTCTCGGGT | 1200 |
| Db | 1141 | attccgatgccttatgcaaaaacttaaccgcgtagctatgagaaggggtcacagctctcgggt | 1200 |
| Oy | 1201 | CMAACCCCTGGACANGTGGCCACTGAGACCTTGAAATTAAAGAGGATGCCATGTCATTGCA | 1260 |
| Db | 1201 | ctaacccccctggacatcgtccacgtagaaccttgaaattaagagatgccatgcatcgtca | 1260 |
| Oy | 1261 | AAGAAATGATTAATGTCGACAGGGTTAAGTCTTTTGAFTGTGTACATTGGCGCTGGACCTGC | 1320 |
| Db | 1261 | aagaaatgatgtatgtcgacagggttaagtcttttgaftgtgttacattggcgcctggacctgc | 1320 |
| Oy | 1321 | AAATAAGTCTCTTTTTCTTCTTAATGAGACAGAAAAATATATGTAATTTTTATATATATGCTA | 1380 |
| Db | 1321 | aaataagtcctcttttcttctaagagagagaaaaatatatgtatcttttataataatgcta | 1380 |
| Oy | 1381 | AAGTTATATTTTCAGTGTATATGTTTCTGTGCAAGTTTGTAAATTATATTTGTGCTAT | 1440 |
| Db | 1381 | aagttatatctcagtgtaatgtttctgtgcaaagtttgtlaatatatatttctgtctat | 1440 |
| Oy | 1441 | AGTATTGTGATTCAAATATTTTAAAAATGCTCACCTGTGACATATTAAGSTTTTAATG | 1500 |
| Db | 1441 | agtatttgtatccaataatttaaataatgtctcactgttgacaattttaaagttttaaag | 1500 |
| Oy | 1501 | TACAGATGATTTAACTGTGGTGACACTTGTGAATTCCTCGTAGAGTACTGTAGCTAAAGGG | 1560 |
| Db | 1501 | tacagatgatatttaactgtgtgcacttctgaatcccttgaaagtlaccctgactagaagggg | 1560 |
| Oy | 1561 | GCAGAACTACTGTTTCTGGTGACCACATGTAAGTTATTCTTTATCTTTTAACTTAATA | 1620 |
| Db | 1561 | gcagaaactactgtttctgtgtaccacatgtagttattcttattcttctaacttaataata | 1620 |
| Oy | 1621 | GAGTCTTCAG 1630 | |
| Db | 1621 | gagctcttcag 1630 | |
| <hr/> | | | |
| RESULT 3 | | | |
| AAD15310 | | | |
| ID | AAD15310 standard; cDNA; 1630 BP. | | |
| XX | | | |
| AC | | | |
| XX | | | |
| XX | AAD15310; | | |
| DT | 15-NOV-2001 (first entry) | | |
| XX | | | |
| DE | Murine receptor activator of NF kappaB ligand (RANKL) cDNA. | | |
| XX | | | |
| KM | Murine receptor activator of nuclear factor kappaB ligand; RANKL; NF; | | |
| KW | tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; | | |
| KW | immune response; inflammatory response; graft-versus-host reaction; | | |
| KW | toxic shock; sepsis; acute inflammatory reaction; bone resorption; | | |
| XX | anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss | | |
| OS | Mus musculus. | | |
| XX | | | |
| FH | Key | | |
| FT | CDS | | |
| FT | Location/Qualifiers | | |
| FT | 3..887 | | |
| FT | /tag= a | | |
| FT | /product= "Murine RANK ligand (RANKL) protein" | | |
| FT | /note= "CDS does not include start codon" | | |
| FT | /partial | | |
| XX | | | |
| XX | US6271349-B1. | | |
| XX | | | |
| PD | 07-AUG-2001. | | |
| XX | | | |
| PF | 17-DEC-1998; 98US-0215649. | | |
| XX | | | |
| PR | 23-DEC-1996; 96US-0059978. | | |

| | |
|----|---|
| XX | (IMMV) IMMUNEX CORP. |
| PI | Dougall WC, Galibert L; |
| XX | WI, 2001-520313/57. |
| DR | P-PSTDB; AA08737. |
| XX | New receptor activator of NF-kappa (RANK) polypeptides, useful for |
| PT | regulating immune response, in screening for RANK inhibitors, or as an |
| PT | adjunct therapy for disease characterized by neoplastic cells that |
| PT | express RANK - |
| PS | Example 7; Column 63-66; 47pp; English. |
| CC | The patent discloses novel receptor activator of nuclear factor (NF)- |
| CC | kappa (RANK) proteins and their corresponding DNAs. RANK is a member |
| CC | of the tumour necrosis factor (TNF) receptor superfamily and associates |
| CC | with TNF receptor associated factor (TRAF) 2 and 3 which are important |
| CC | in the regulation of immune and inflammatory response. The receptors |
| CC | are useful for regulating immune response and in screening for inhibitors |
| CC | of these receptors. The cytoplasmic domain of RANK is used in developing |
| CC | assays for inhibitors of signal transduction, e.g. for screening the |
| CC | molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, |
| CC | TRAF5 and particularly TRAF6. NF-kappa inhibition by RANK antagonists |
| CC | are useful in ameliorating the negative effects of an inflammatory |
| CC | response that result from triggering of RANK, e.g. in treating toxic |
| CC | shock or sepsis, graft-versus-host reactions, acute inflammatory |
| CC | reactions and the effects of bone resorption. RANK acts as an anti- |
| CC | apoptotic signal and rescue the cells that express RANK from apoptosis. |
| CC | Soluble forms of the receptor are used in vivo or in vitro based |
| CC | screening tests for agonists or antagonists of RANK activity, as |
| CC | antagonists of RANK-mediated NF-kappa B activation, or to inhibit |
| CC | transduction of a signal via RANK. RANK compositions are used in the |
| CC | development of both agonistic and antagonistic antibodies, or as an |
| CC | adjunct therapy for disease characterised by neoplastic cells that |
| CC | express RANK. Compounds that interfere with RANK/TRAF6 interactions |
| CC | are useful for modulating the formation of osteoclasts from osteoclast |
| CC | precursors and for modulating osteoclast function and activities. They |
| CC | are used as inhibitors of diseases associated with excess bone resorption |
| CC | and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are |
| CC | useful for the expression or distribution of recombinant proteins, as probes for analysis |
| CC | of the presence or distribution of RANK transcripts, while the proteins |
| CC | are useful in preparing kits for the detection of soluble RANK, or |
| CC | monitor RANK-related activity. The present sequence is a cDNA encoding |
| CC | murine RANK ligand (RANKL) protein. |
| XX | |
| SQ | Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other: |
| YY | Query Match 100.0%; Score 1630; DB 22; Length 1630; |
| | Best Local Similarity 100.0%; Pred. No. 0; |
| | Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0 |
| DB | 1 CGGCGCTCCACACAGAGGTCCGCTGCACCOCGGCCTTTCGACCGGCTCGGGCCGCC 60 |
| | |
| DB | 1 ccgagctccacacagagggtccgctgcaccoccgagccttcgtacccggatcggcgcgcg 60 |
| YY | 61 CACCGCGCGGCTCCCGCTCATGTTCTCTGGGCCCTCTCTGGGGCGGAGCAATGAGTG 120 |
| | |
| DB | 61 caccgcgcgcctccgcgtccaagtcccgcgcctccttggggcgcatcgggacggcgagtg 120 |
| YY | 121 TCTGCAGCATCGCTGTTCTGTTACTTTGAGCGCAGATGATCTTAACAGAAATTCAG 180 |
| | |
| DB | 121 tcctgcagcatcgctgtcttccgtactttccgagcgagatggattcctaagaatatcag 180 |
| YY | 181 AGACAGCACTACTGCTTTTATAGAATCCTGAGACTCCATGAAGAACGAGATTTCAG 240 |
| | |

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Db 181 aagacgcacctcacctcttcttaagaa tccctgagactcca tgaaaacgcaga ttctgcag 240
Oy 241 ACTCGACTCTGGAGACTGGAAGACACACTACTGACTCTCTGAGAGAGATGAACAAGCCT 300
Db 241 aatcgcctctctgagagctgaaagacaacactccctgactccctgcagggagatgaaacaagcct 300
Oy 301 TTCAGGGGGCCCTGCCAAGAAAGAACTGCACAACTTGTGGGGCCACAGCCCTTCTCAGAG 360
Db 301 tctcagggggccgctgcagaaagaaactgcaacacatctgtgaggccacagcgtctctcagag 360
Oy 361 CTCACGCTTGTGATGGAAGGCTCATGGTTGGATGTGGCCAGGAGAGCAAGCTGAGGCC 420
Db 361 cctcagcctctctgagagagctcca tggctgtgagctgcagccagcagagcctctgagccc 420
Oy 421 AGCCATTTTGCACACCTCACCATCAATGCTGCAGCATCCCATCGGGTTCCCTAAAGTCA 480
Db 421 agccatttgcacacctccaacatcaatctgcgcagcatcccatcgggttccca taaagcca 480
Oy 481 CTCTGCTCTTGTGTACCAACGATCGAGGCTGGGCCAAGATCTCTTAACATGACGTTAAGCA 540
Db 481 cctctgctcctctgtgacacagctcgagggctggccaaagatctctaaactgaagctaaagca 540
Oy 541 ACGGAAACTAAGGCTTAACCAAGATGGCTTCTATTACCTGACGCCAACAATTTGCTTTC 600
Db 541 acggaaactaagggtttaaaccagaatctctctctctctacccctgtaagccaacatctgcttc 600
Oy 601 GGCATCATGAACATCGCGAAGCGTACCTACAGACTATCTTCACTGATGTTATGTCG 660
Db 601 ggcatacctgaacacacgcggaagcgtacctaagacta ccttcaagctgtgtgtatgtctgc 660
Oy 661 TTTAAACCAAGCATCAAAATCCCAAGTTCATTAACCTATGAAGAGAGGAGGACGAA 720
Db 661 ttaaaacacagcatcaaaatcccaagctctcctaaactgaacgtgaaggaaggaacgaa 720
Oy 721 ACTGCTCGGGCAATTTCTGAATTTCCACTTTTATTCATTAATGTTGGGGATTTTCAAGC 780
Db 721 actgctcgggcaatctctgaaatctcactctta tcaataaagcttgggggacttttccaagc 780
Oy 781 TCCGAGCGTGTGAAGAAATTAGCATTCAGGTGTCAACCCCTCCCTGCTGATCCGGATC 840
Db 781 tccgagcggtgtgaagaaattagcatctcagcttccaaacctctcctgtgtatccgagctc 840
Oy 841 AAGATGCGAGCTACTTTTGGGCTTTCAAAGTTCAGAGCATAGCATGACACTATTTGCTG 900
Db 841 aagatgcgagctacttttgggcttctcaaaagcttcaggacaatgactgaagcccatctcgtg 900
Oy 901 GAACATTAGCATGTGATGCTCTAGATGTTTGAACCTTCTTAAAAAATGATGATGCTAT 960
Db 901 gaacatttagcatgtgattgctctagatgttctgaaactctttaa aaatgactgactat 960
Oy 961 ACATGCTTAAGACTACTTAAGAGACATGGCCACCGCTGTATGAACCTCACAGCCCTCTCTC 1020
Db 961 acatgcttaagactactttaagagacatggccacgcgtgtatgaacctcacagccctctctc 1020
Oy 1021 TTGAGCCCTGTACAGTGTGTATATGTAAGTCCATAGTATGATGATGATGATGAT 1080
Db 1021 ttgagccctgtacaggttctgtatata tgtaaagctccatagtgatgtatcattcagtgat 1080
Oy 1081 TACACACAGGTTTTACATTTTGTAAATGATTTCTTACAAATGAACAAGATTGGAGAGT 1140
Db 1081 tacacacaggttttacatcttctgaatgattccttagaatgaaacagatctggaagagct 1140
Oy 1141 ATTGCGATGCTTATGA AAAAATTACAGTGTGATGATGAAGGGGTGACAGTCTCTGGGT 1200
Db 1141 attcgatgcttattga aaaaattacaggtgtgattgaaggggtgacaggtctctcctgggt 1200
Oy 1201 CTAAACCCCTGGACATGTGCCACTGAGAACCTTGAATAATTAGAGAGATCCATGTCTATGCA 1260
Db 1201 cttaaacctctgacatgtgccactgaaaccttgaaatlaagagatgcatgtcatgtgca 1260
Oy 1261 AAGAAATGATGTGTGAAGGTTAAGTCTTTTGAATTTGTACTTTCGCTGGGACCTGC 1320
Db 1261 aagaaatgattgtgtgaaggtttaagcttcttctgaatcttgaactgtcaactgtcgtaacctgc 1320

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Oy 1321 AAATAGTTCTTTTTTCTTATAGAGAGAGAAATATATGATATTTTATTAATGCTTA 1380
Db 1321 aaataagttctttttcttata tgaagagaaaaataatglatttatataataatgtctta 1380
Oy 1381 AAGTTATTTTCAGGTGAATGTTTCTGTGCAAAAGTTTGTAAATTAATTTGTGCTAT 1440
Db 1381 aagttatcttcaaggtgataatgtttctgtgcaaaagtttctgtaaatatataatctgtctat 1440
Oy 1441 AGTATTTATTTCAAAATATTTTAAAAATGCTCTCACTGTTGACATATTTAATGTTTAAATG 1500
Db 1441 agtatcttcaaaaataatcttaaaaatgtctcactgtgtacatatataatcttcttaaaatg 1500
Oy 1501 TACAGATGATTTTAACGTGCTGCTACTTTGTATTTCCCTGGAAGTACTGTAAGCTAATA 1560
Db 1501 tacagatgattttaacgtgctgctactttgtat tttccctggaagtactgtaagcttaag 1560
Oy 1561 GCAGAAATACGTTTCTGTGACACATGATGTTTATTTCTTTATTTCTTTAACTTAATA 1620
Db 1561 gcagaatactgttctgtgacacatgattgtttat tttctttcttcttcttcttaactaata 1620
Oy 1621 GAGTCTTCAG 1630
Db 1621 gagtcttcag 1630

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RESULT 4

AAD08714
ID AAD08714 standard; cDNA; 1630 bp.

AC AAD08714;
DT 04-SEP-2001 (first entry)
XX

DE Murine receptor activator of NF- κ B ligand (RANKL) cDNA.

XX Murine: receptor activator of NF- κ B; RANK; tumour necrosis factor;
KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
KM chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein; 89.
XX Mus musculus.

OS
XX
FH Location/Qualifiers
FT 3..887
FT CDS
FT /*tag= a
FT /product= "Murine RANKL protein"
FT /note= "CDS does not include start codon"
FT /partial

XX US6242213-B1.

XX 05-JUN-2001.

XX 22-DEC-1997; 97US-0995659.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0077181.

XX 14-OCT-1997; 97US-0064671.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM;

XX WPI; 2001-407216/43.

XX DR P-PSDB; AAE04425.

XX New DNA molecules, useful for producing ligands (which are useful for
PT regulating immune response and in screening for inhibitors of NF- κ B
PT receptor activator) of the receptor activator of NF- κ B (RANK) -
XX Example 7; Column 57-60; 43pp; English.
XX The present invention relates to receptor activator of NF- κ B (RANK)

CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
 CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
 CC proteins respectively. RANK is a member of the tumour necrosis factor
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
 CC and TRAF3. The DNA molecules with TNF receptor-associated factor (TRAF) 2
 CC ligands are useful for regulating immune response and in screening
 CC for inhibitors of RANK. The present sequence is murine RANKL cDNA.
 XX
 SQ Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Query Match 100.0%; Score 1630; DB 22; Length 1630;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGTCCACAGAGGCTCCGTGACCCCGCCTTCTGACCGGCTCCGGCGCCG 60
 Db 1 cggggtccacaagaggtccgtgcaccccgcttcgcaacggctccggcgccgc 60
 QY 61 CACCGCGCCTCCCGCTCCATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 Db 61 caccgcgctcccgctcccaatgttcctcgtggtggtggtggtggtggtggtggtg 120
 QY 121 TCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 Db 121 tctgagatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 180
 QY 181 AAGAGCAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 181 aagagcagctactgctgctgctgctgctgctgctgctgctgctgctgctgctg 240
 QY 241 ACTGCACTCTGGAGAGTGAACACACACTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 Db 241 actgcactctggagagtgtaagacacactgctgctgctgctgctgctgctgctg 300
 QY 301 TTCAGGGGCGCTGCGAGAGAGAACTGAGAACTGAGAGAGAGAGAGAGAGAGAG 360
 Db 301 ttcaaggggcgctgcagaaagaaactgcacaacatgtggtggcgacagcgcttc 360
 QY 361 CTCGAGTATGATGAGAGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 361 ctccagatgtagtgaagctcatgtgtggtggtggtggtggtggtggtggtggtg 420
 QY 421 AACCATTTCACACCTCACCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Db 421 agccatttcacacctcacccacacacacacacacacacacacacacacacacac 480
 QY 481 CTCTGCTCTTGTGCTACGAGATGAGGCTGAGGCAAGATCTCTAATGAGCTTA 540
 Db 481 ctctgctcttgtgctacgagatgagggctgagggccaaagatctctaatacgt 540
 QY 541 ACGGAAACTAAGGCTTAACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 Db 541 acggaactaagggcttaaccaaagatgctcctacacacacacacacacacacac 600
 QY 601 GGCATGATGAACATGCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 601 ggcataatgaacatcggaaggctgctcctacacacacacacacacacacacac 660
 QY 661 TTAACAACGACATCAAAATCCAAAGTTCATTAACCTGATGAAGAGAGAGACA 720
 Db 661 ttataaacgacatcaaaatcccaagttcatacctgataaagagagagacgaaaa 720
 QY 721 ACTGCTCGGGCAATTCTGAATTCCTATTTATTCATTAATGTTGGGGGTTTTC 780
 Db 721 actgctcgggcaatttctgaattcctattatccataaagtgtggggatcttcaaac 780
 QY 781 TCCGAGTGGTGAAGAATATGACATTCAGGTGTCACACCTTCCCTGCTGATCC 840
 Db 781 tccgagctggtgaagaatattgacattcaggtgtgccaaaccttccctgctgac 840
 QY 841 AAGATGCGAGTACTTGGGGCTTTCAAAAGTTCAGGACATAGACTCAITTCG 900

Db 841 aagatgagcagctacttgggtgttcaagttcagagacataagactgacatctcgtg 900
 QY 901 GAACATTAGATGAGATGCTCCTACATGCTTTGGAACCTTTAAATAATGATGATGCTAT 960
 Db 901 gaacattagatgagatgctcctacatgcttttggaaactcttaaaatgatgactat 960
 QY 961 ACATGTTAGACTACTAAGAGACATGAGCCACGAGTGTATGAAGCTCACAGCCCTCTC 1020
 Db 961 acatgttaagactactaagagacatgagccacgagtgatgaactcaacagccctctc 1020
 QY 1021 TTGAGCTGTACAGGTTGTATATGTAAGTCCATAGCTGATGATGATGATGATGAT 1080
 Db 1021 ttgagctgtacagggtgtgtatgtatgaagttccatagatgagatgagatgagat 1080
 QY 1081 TACACAGGCTTTTACAAATTTGTAATGATTTCTGATGANTTGAACAGATTTGGAGAG 1140
 Db 1081 tacacaggcttttacaaatttgtaatgatttctgaatgagacagatgtggagag 1140
 QY 1141 ATTCCGATGCTTATGAATAAATTACAGCTGAGCTATGGAAGGGGCTCACAGTCTG 1200
 Db 1141 attccgatgcttatagaataaacttacacgctatgtagaagggtgacagctctggt 1200
 QY 1201 CTAAACCCCTGACATGTCGCCACTGAGAACTTGAAATTAAGAGATGCCATGCTATGCA 1260
 Db 1201 ctaaaccttgacatgctgccactgagaaacttgaaatgaagagagatgcatgtgca 1260
 QY 1261 AAGAAATGATGATGTAAGGCTTAAGTTCCTTTGTAATGTTGTTACATTCGCTGGAC 1320
 Db 1261 aagaaatgatgatgtgaaggcttaagtcttctgtaattgtttacatctgcgtggac 1320
 QY 1321 AAATAAGTCTCTTTTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 Db 1321 aaataagtctcttttcttaatagagagagagagagagagagagagagagagagag 1380
 QY 1381 AAGTTATTTTCAGTGAATGTTCTGCTGCAAGTTTGTAAATATATTTGCTAT 1440
 Db 1381 aagttattttcagtgaatgttctgctgcaagtttgtaaatatttttctat 1440
 QY 1441 AGTATTTGATCAAAATTTTAAATAATGCTCAGCTGTTGACATATTAAATGTTTAA 1500
 Db 1441 agtatttgatcaaaatttttaaataatgctcagctgtgacatatttaattgaa 1500
 QY 1501 TACAGATGATTAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 Db 1501 tacagatgatattaatgaagtgtgctgctgctgctgctgctgctgctgctgctg 1560
 QY 1561 GCAGATGCTGTTGCTGACACATGATGATTTATTTCTTATTTTAACTAATA 1620
 Db 1561 gcagatgctgttctgacacatgattttattttcttatttttcttacttaata 1620
 QY 1621 GAGTCTCAG 1630
 Db 1621 gagtctcag 1630

RESULT 5
 AAD05903
 ID AAD05903 standard; cDNA; 1630 BP.

AC AAD05903;

DT 31-JUL-2001 (first entry)

DE Murine RANKL (receptor activator of NF-kappaB ligand) cDNA.

XX Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;

KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;

KW TNF receptor associated factor; TRAF; RANK ligand; RANKL; osteopathic;

KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;

KW immune system dysfunction; familial expansile osteolysis; FEO;

KW early onset Paget's disease of bone; EP; cytoskeletal; ss.

| | |
|----|--|
| OS | Mus musculus. |
| XX | |
| XX | Key |
| XX | Location/Qualifiers |
| FT | 3..887 |
| FT | /*tag- a |
| FT | /product= "Murine RANKL (receptor activator of |
| FT | NF-kappaB ligand) protein" |
| XX | |
| PN | MO200136637-A1. |
| XX | |
| PD | 25-MAY-2001. |
| XX | |
| XX | 14-NOV-2000; 2000MO-US31459. |
| XX | |
| PR | 17-NOV-1999; 99US-0442029. |
| XX | |
| PA | (IMMV) IMMUNEX CORP. |
| XX | |
| PI | Anderson DM, Hughes AE; |
| XX | |
| DR | WPI; 2001-329222/34. |
| DR | P-PSDB; AAEO1992. |

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the
PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
XX
PS Example 7; Page 72-74; 56pp; English.

PS Example 7; Page 72-74; 96pp; English.

XX

CC The present invention relates to a novel receptor, referred to as RANK

CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF

CC (tumour necrosis factor) receptor superfamily. RANK is a Type I

CC transmembrane protein that interacts with TNF receptor-associated

CC factors (TRAFs). Triggering of RANK by overexpression or co-expression

CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation

CC of the transcription factor NF-kappaB, a ubiquitous transcription factor

CC that is most extensively utilized in cells of the immune system.

CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating

CC negative effects of inflammatory reactions, and the effects of excess

CC bone resorption. The RANK DNAs, proteins and their analogues are useful

CC for the preparation of pharmaceutical compositions, for infecting target

CC cells for use in gene therapy applications in diagnosing diseases

CC associated with RANK, and as targets for use in screening assays. They

CC may be used in the treatment or diagnosis of immune system dysfunction.

CC The present invention also encompasses gene therapy methods to correct

CC gene-activating mutations, associated with e.g. familial expansile

CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The

CC present sequence is a cDNA encoding murine RANKL (murRANKL) protein.

XX

Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

| Query Match | 100.0% | Score 1630 | DB 22 | Length 1630 |
|-----------------------|---|--------------|----------|-------------|
| Best Local Similarity | 100.0% | Pred. No. 0 | | |
| Matches 1630 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY 1 | CCGGCGTCCACACAGAGGTCGCGTGCACACCCGGCGCTTCGACACGGCTCCGGGCGCG | 60 | | |
| Db 1 | cggggtcccaacagaggggtccgcgcgacccgccttcgcgcacgcggtccgcgcgcgc | 60 | | |
| QY 61 | CACCCGCCCTCCCGCTCATGTTCTGAGCCCTCTGGGGCTGGGACATGGGCAAGTGG | 120 | | |
| Db 61 | caccgcgcctccgcctccatcgtcttcgcgcctcctcctggtggtcgtgacgtgcgcggtg | 120 | | |
| QY 121 | TCTGAGACATGCGCTCTGTTCTCTGTACTTTCCAGGCGCAGATGCATCTTAACAAATTCAG | 180 | | |
| Db 121 | tctgtagatcgtcttgcctcgttactcttcgcgcgcagcagatgactcttaacagaataatcg | 180 | | |
| QY 181 | AAGACAGACATCATGCTTTTATAGAAATCCTAGACTCCATGAAAAACGAGATTGGCAGG | 240 | | |
| Db 181 | aagacagacatcatcgccttcttaagaaatccctgcgcgtcccaatgaacgcagatctgcagg | 240 | | |
| QY 241 | ACTGCAGCTCTGGAGAGTGAAGACACACTACCTGACTCTCTGCAGGAGATGAANAACAGCT | 300 | | |

| | | | | | | | | | | | | | | | | | | |
|----|------|-------------|-------------|------------|-------------|-------------|------------|-------------|------------|-----------|---------|--------|-------|--------|------|------|-----|------|
| Db | 241 | actgcactctc | gagagatg | gaagacacac | ctcctg | aactctc | gcagagga | tgaaacaagcc | 300 | | | | | | | | | |
| Oy | 301 | TTCAAGGGG | CCGTGCAGAGA | GAACATGC | CAACACATTTG | GGGGCCACAG | CGCTTCTCAG | AGAG | 360 | | | | | | | | | |
| Db | 301 | ctcaagggg | ccgctgcagaa | gaagaa | actgtaacac | atgctg | tggggcca | caagcgctctc | taagag | 360 | | | | | | | | |
| Oy | 361 | CTCCAGCT | ATGATGTGA | AGGCTCAT | GGTGTGGAT | GTGGCCACG | AGAGCAAG | CTTAGAGCC | 420 | | | | | | | | | |
| Db | 361 | ctccagactat | gatlgaag | agctcat | gtgtg | atgtg | gtgcccag | cgagcgcc | ctgcgccc | 420 | | | | | | | | |
| Oy | 421 | AGCCATT | TGGCACCTC | ACCATCAT | AAGTCTCC | GCAGATCCCAT | CGGGTTC | CCATAAAGCA | 480 | | | | | | | | | |
| Db | 421 | agccatttgc | acaccc | ctccac | ctcaaa | tgctgc | agagcc | atccca | tcgggtctcc | taaaagta | 480 | | | | | | | |
| Oy | 481 | CTTGCTC | CTTTGGTAC | CAGATCGA | GGCTGGG | CCCAAGATCT | CTAATCAG | ATGAGCTTA | AGCA | 540 | | | | | | | | |
| Db | 481 | ctctgctct | cttctgtt | accacga | ctcgag | cgctgggcca | gaatctct | taacat | tgaaagct | taagca | 540 | | | | | | | |
| Oy | 541 | ACGGAAC | TAAAGG | GTAAACCA | AGATGGCTT | CTATTAC | CTGACGCC | CAACATTTG | CTTTG | 600 | | | | | | | | |
| Db | 541 | acggaaac | taeaggt | ctaaacca | agaatg | ctctcat | taacgt | ctagcaca | aatctgctc | 600 | | | | | | | | |
| Oy | 601 | GGCAT | TCATGAAC | TTCGGGAA | GGGTAC | TCTCATAC | ATCATTTCA | CGATGAGT | GTATG | 660 | | | | | | | | |
| Db | 601 | ggcatc | atgaaac | tcgggaag | cgctac | ctcctc | agactat | ctcaag | ctgtagt | gtatg | 660 | | | | | | | |
| Oy | 661 | TTTAAAC | CCAGCAT | CAAAATCC | CAAGTTCT | CTATTAAC | TGATGAAG | AGAGGAG | GCACAGAA | 720 | | | | | | | | |
| Db | 661 | ttaaacc | agatata | aaaaatcc | caagtct | ctatac | tatc | atgtaag | ggagggca | agaaaa | 720 | | | | | | | |
| Oy | 721 | ACTGCTG | GGGCATTT | CTGAATTC | CACTTTT | ATTCCAT | TAATGTT | GGGGATTTT | TTTCA | 780 | | | | | | | | |
| Db | 721 | actgctg | gggcaat | ctcgaa | ttccact | ttatcc | ataa | ctgtgg | gggattct | ccaagc | 780 | | | | | | | |
| Oy | 781 | TCCGCG | CGGGGA | GAATTA | AGATTCAG | TTCAGTTC | CAACCTTCC | CGTGGAT | CCGGATC | 840 | | | | | | | | |
| Db | 781 | tcgagc | ggygaag | aaatct | agatct | aaagctg | ctccaa | ccctctcc | gctgga | ctccgagct | 840 | | | | | | | |
| Oy | 841 | AAGAT | TGGACG | TACTTTT | GGGGCTT | TTCAAAT | TTCAGAC | ATAGACT | GTAGACT | CTATT | 900 | | | | | | | |
| Db | 841 | aagat | tgagc | gtactct | tggggct | cttcaaa | gtctag | gaac | tagac | tagac | ctcaat | 900 | | | | | | |
| Oy | 901 | GAACTTA | TGATGAT | GTCTT | AGATGTTT | TGGAAAT | CTTCTT | AAAAAAT | TGATGAT | GTCTAT | 960 | | | | | | | |
| Db | 901 | gaacat | taagat | gtatg | ctctag | atgctt | tgaaac | ctctta | aaaaat | tgatg | atgctat | 960 | | | | | | |
| Oy | 961 | ACATG | TGTGA | GACTAC | TAAAGAC | ATGAGC | CGCCAC | AGGTGTAT | GAATCA | CACAGCC | CTCTC | 1020 | | | | | | |
| Db | 961 | acatg | tgatga | gactac | taagac | atgagc | atgagc | atgagc | atgagc | atgagc | atgagc | 1020 | | | | | | |
| Oy | 1021 | TTGAG | CCCTG | TACAG | GTGTGTAT | ATGTAAT | GAAGTCC | ATAGG | GTATG | TATGAT | TCATG | 1080 | | | | | | |
| Db | 1021 | ttgagc | ctgac | aggtgt | gtatg | tata | gtataa | gtccat | aggtgt | atg | atg | 1080 | | | | | | |
| Oy | 1081 | TACACA | CGGTTTT | TACAATTT | TGTAATG | ATTTTCT | TGAATTA | AGACAG | ATTTGG | GAGAG | AG | 1140 | | | | | | |
| Db | 1081 | tacaca | cggttt | tacaatt | ttgt | taatgt | atctt | ctagaa | ttgaa | ccaggt | ctg | ggaggg | 999 | 1140 | | | | |
| Oy | 1141 | ATTCCG | ATGCTTAT | GA AAAA | CTTACAC | GTGAGCT | ATGAAAG | GGGGCT | CACAG | CTCTG | GGT | 1200 | | | | | | |
| Db | 1141 | attccg | atgctt | atgtaaaa | cttacc | gtacg | tgagct | atgaa | ggggg | gtc | aaagct | ctc | gggt | 1200 | | | | |
| Oy | 1201 | CTAAC | CCCTG | ACACTG | CGCAC | TGAGAC | CTTAAAT | TAAAG | AGATG | CCCATG | TCAT | TGCA | 1260 | | | | | |
| Db | 1201 | ctaa | ccctg | acag | ctg | gacac | tgaa | ac | ctg | aaat | taag | ggatg | cca | tgctat | gca | 1260 | | |
| Oy | 1261 | AAGAA | TGATAG | TGTGA | AGGTTA | AGTTCTTT | TGGAATTT | CTTAC | TATG | CTTG | CGCTGG | AC | CTGC | 1320 | | | | |
| Db | 1261 | aagaa | tga | tatg | atg | tggaagg | gttaag | gttctt | ctg | aaat | tgta | cat | ctg | cg | ctg | ggcc | ggc | 1320 |
| Oy | 1321 | AAAT | TAAGTCT | TTTTTT | CTAT | ATAGAG | AGAAATAT | ATATAT | GTATTT | TATAT | TATAT | AT | GTCTA | 1380 | | | | |
| Db | 1321 | aaat | taag | tctctt | cttctt | ctata | tgagga | gaaaaa | tata | tgta | cttctt | ctata | taaa | tgctca | 1380 | | | |


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Oy 781 TCCGAGCTGTGTAAGAAATTACATTCAGGTGTCCACCCCTCCCTGCTGATCCGGATC 840
    |||||||
Db 1002 tccggagctgtgtaagaaattacatctcaggtgtccaaacctccctgctggtccggatc 1061
Oy 841 AAGATGCGACGACTTTGGGCGCTTCAAGATGACAGATGACAGATCATTTCTGTG 900
    |||||||
Db 1062 aagatgacgacgactttgggctgttcaagatgacagatgacagatcatcttcgtg 1121
Oy 901 GAACATTAAGCATGATGATGCTGATGATTTGGAAACTCTTAAATAATGATGATGCTAT 960
    |||||||
Db 1122 gaacattagcatgatagtgtccctagatgttggaaacttcttaaaaaatgatagtctcat 1181
Oy 961 ACATGTGTAAAGCTACTAAGAGACATGGCCACGCTGATGAAACTCAGCCCTCTCTC 1020
    |||||||
Db 1182 acatgtgtaaagctactaagagacatggccacggtgtatgaaactcagccctctctc 1241
Oy 1021 TTGACCCGTGACAGTGTGTATGTAAGTCATAGTATGATGATGATGATGATGATGAT 1080
    |||||||
Db 1242 ttgagccgtacaggtgtgtatataatgacacaggtgagtgatgatactatgagtgat 1301
Oy 1081 TACACAAAGGTTTTACAATTTTGTAAATGATTTCTAGAAATGAAACAGATTTGGAGAGT 1140
    |||||||
Db 1302 tacacaaggttttacaattttgttaattgtatcctcctagaaattgaaacagattggagaggt 1361
Oy 1141 ATTCCGATGCTTATGAAAACTTACAGCTGAGCTATGGAAGGGGCTCAGCTCTGTGGGT 1200
    |||||||
Db 1362 attccgagcttataagaaaaactacacgtgagctatgaaagggtgtccacagctctctggt 1421
Oy 1201 CTAAACCCCTGGACATGCTCCACTGAGACCTTGAATTAAGAGATGGCATGATGATGCA 1260
    |||||||
Db 1422 ctaaaccttggacatgtgtccactggaaccttgaaatcaagagatgacatgcatgtgca 1481
Oy 1261 AAGAAATATATAGTGTGAAGGTTAAGTTCTTTGAAATGTTACATTTGGCTGGAGACTGC 1320
    |||||||
Db 1482 aagaaatatagtgtgaagggttgaagttcttcttgaaattgtacactgtgcgtggagaccgc 1541
Oy 1321 AAATAGTCTTTTCTTTCTTATGAGAGAGAGAAAAATATATGATTTTATTTAATGTCTA 1380
    |||||||
Db 1542 aaatagctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1601
Oy 1381 AAGTTATATTTTACAGTGAATGTTTCTGTGCAAAAGTTTGTAAATTTATTTGAGCTAT 1440
    |||||||
Db 1602 aagttatatttcagagtgtaagttcttctgtgcaaaagtcttcttcttcttcttcttcttct 1661
Oy 1441 AGTATTTATTTCAAAATATTTTAAATGTCTTCTGATGATTTTAAATGTTTAAATG 1500
    |||||||
Db 1662 agtatttcttcaaaaattcttcaaaaattcttcaaaaattcttcaaaaattcttcaaaa 1721
Oy 1501 TACGATGATTTTAAAGTGTGACCTTTGATTTCCCTGGAAGTACTGCTAAGGGG 1560
    |||||||
Db 1722 tacgagatgatttaaacgtgtgacacttcttcttcttcttcttcttcttcttcttcttct 1781
Oy 1561 GCAGAAATACTGTTCTGTGTGACGACATGATGATTTATTTCTTATTTCTTTAACTTATA 1620
    |||||||
Db 1782 gcagaaatactgttctgtgtgacacatgtagttcttcttcttcttcttcttcttcttct 1841
Oy 1621 GAGCTTTACG 1630
    |||||||
Db 1842 gagcttctcag 1851

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RESULT 7
AA299966
ID AA299966 standard; DNA: 2299 BP.
XX
AC AA299966:
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding a murine osteoprotegerin ligand (OPGL).
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;

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KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 170..1120
FT /tag="a
FT /product="osteoprotegerin ligand"
XX
PN M0200015607-A1.
XX
PD 23-MAR-2000.
XX
PE 13-SEP-1999; 99MO-DK00481.
XX
PR 15-SEP-1998; 98DK-0001164.
PR 02-OCT-1998; 98US-0102896.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Halkier T, Haaning J;
XX
DR WPI: 2000-271444/23.
DR P-PSDB; AAY84419.
XX
PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
PT to treat, prevent and ameliorate osteoporosis -
XX
PS Disclosure; Page 82-85; 110pp; English.
XX
CC The present sequence encodes a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.
XX
SQ Sequence 2299 BP; 641 A; 494 C; 541 G; 623 T; 0 other;

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Query Match 99.9%; Score 1628.4; DB 21; Length 2299;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 CGCGGCTCCACACAGAGGTCGCCGTGACCCGCGCTTCTGACCGCGCTCGGCCCGC 60
    |||||||
Db 234 cggcggtccacacagaggttcgctgcacccgcgcttctgacccggtccggtccggtccg 293
Oy 61 CACCGCGCGCTCCGCTGATGTTCTGCGCTGCGGGGCGGAGCTGAGGCGCAGAGTGG 120
    |||||||
Db 294 caccgctcgctccgctccatgttccgtccctccgtggagctgggacgtgggacaggtgg 353
Oy 121 TCTGACGATGCTGCTGTTCTGCTGACTTTGAGCGGACGATGATCTTAAACAGATTTGCAG 180
    |||||||
Db 354 tctgacgactgtctgttctctgttcttctgagcgtgagatgagatctcttaacagatatcag 413
Oy 181 AAGACAGACTCAGCTGTTTATGAAATCTGTGAGACTCCATGAAACGACGATTTGCAG 240
    |||||||
Db 414 aagacagactcagctgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 473
Oy 241 ACTGCACTGTGAGAGTGAAGACACTGACTGCTGACGAGAGAGTGAAGAAACAGCTT 300
    |||||||
Db 474 actgactctgagagatgaaagacactactcgtactccctgcagagagatgaaacagacct 533

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OY 301 TTTCAGGGGCGCGTGCAGAGAACTGCACACATTGTGGGGCCACAGCGCTTCAGAG 360
Db 534 ttcaggggcccgtgcagagaaactgcacacattcgtggggccacagcgcttcacagga 593
OY 361 CTCAGCTATGATGAAGGCTCATGTGTGGATGTGGCCACGAGGCAAGCCTGAGGCC 420
Db 594 ctccagctatgatagtgaaggtccatcgtgtggtggtccagcgaggaagctgaagccc 653
OY 421 AGCATTGGACACCTCCACATCAATGCTGCACATCCCATCGGGTCCATTAATCA 480
Db 654 agccatttgcacacctcaaccatcactgtccagcattcccatcgggtccataaagltca 713
OY 481 CTCGTCTCTTGTGACAGATGAGGCTGGGCCAAGATCTCAACATGACGCTTAAGCA 540
Db 714 ctctgtctcttctgttacacagatcgaagcgtggccaaagatctcacaatgscgtlaagca 773
OY 541 ACGGAAACTAAGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCTTC 600
Db 774 acggaataactaagggttaaccagaatgcttctattaccctgaacgccaacattgcttcc 833
OY 601 GGATCATGAAACATCGGGAAGCGTACTACAGACTATCTTCAGCTGATGGTGTATGTCG 660
Db 834 ggcatacatgaacaacatcggaaagcgtactacagactatcttcagctgaatggtatgctcg 893
OY 661 TTAATAACAGCATCAAAATCCCAAGTTCATTAACCTGATGAAGAGAGAGACAGAA 720
Db 894 ttaaaacagcatcaaaatcccaagttctcataaccctgaatgaaggaagggagcaagaaaa 953
OY 721 ACTGTGCGGGCAATTCTGAATTCACCTTTATTCATTAATGTTGGGATTTTCAAGC 780
Db 954 actgtcggcgcaattctgaattccacttattcacaatagtgtgggatttttcaagc 1013
OY 781 TCCGAGCTGTGAATAAATTACATTCAGTGTCCAACTCCCTCGTGGATGCCGATC 840
Db 1014 tccgagctgtgtgaagaattagcatcaggtgtccaaacctccctcgtgtccggatc 1073
OY 841 AAGATGCGACGTACTTGGGGCTTCAAAAGTTCCAGAGACATAGACTGAGACTATTCGTG 900
Db 1074 aagatgacgacgtacttggggcttccaaagttccaaagttcagactagacgtgactcatctcg 1133
OY 901 GAACATTAGCATGATGTCCTAGATGTTGGAACTCTCTTAATAAATGATATGTCAT 960
Db 1134 gaacattagcatgattgtctcctagatgttggaaacttcttaaaaaatgatagtctcat 1193
OY 961 ACATGTGTAGACTACTAGAGACATGCGCCAGGCTGTGAACATCAACGCCCTCTCTC 1020
Db 1194 acatgtgtagactactactaagaacatgcccaggtgtatgaactcaacgccctctctcc 1253
OY 1021 TTGAGCCTGTACAGTTGTGTATGTAAAGTCCATAGGTGATGTTAGATTCATGCTGAT 1080
Db 1254 ttgagcctgtacaggttgtgtatgttaaagttccatagtgatgttagatltcatggtgat 1313
OY 1081 TACACAAGCGTTTACAATTTTGTATGATTTCTTGAAATTTGACACAGATTGGAGAGGT 1140
Db 1314 tacacaagcgtttacaattttgtatgtatcttcctagaattgaccagatltggagagaagt 1373
OY 1141 ATTCGATGCTTATGAAAACTTACACGTGAGTATGGAAGGGGTCACAGTCTCGGGT 1200
Db 1374 attccgattgcttatgaaaaacttaacacgtgagctatggaaggggtcacagctctcgggt 1433
OY 1201 CTAAACCCCTGACATGTGCCTAGAGAACCTTGAATTAAGAGGATGCCATGTCTATGCA 1260
Db 1434 cttaacccctgacatgtgcctagagaaacttgaatlaagagatgcccattgtcga 1493
OY 1261 AAGAAATGATGTGTAAGGGTTAAGTTCTTTGAATTTGTAATGTCGCTGGACCTGC 1320
Db 1494 aagaatgatgtgtgaagggttaagttcttttgaattgttaacatgtgcgttggacctgc 1553
OY 1321 AAATAAGTCTCTTTTCTAATGAGGAGAGAAAATATATGATTTTATATATGCTTA 1380
Db 1554 aaataagttcttcttcttaagaggagaaaaataatatagtattttataataatgtctta 1513
OY 1381 AAGTTATATTCAGTGCTAATGTTTCTGTGCAAAAGTTTGTAAATTAATTAATTTGTCTAT 1440

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Db 1614 aagttatattcagtgtaatgtttctgtgcagaagtttgttaataataattgtgctat 1673
OY 1441 AGTATTTGATCAAAATATTAAAAATGCTCACTGTGCATATTTAAATGTTTAAATG 1500
Db 1674 agtatattgatacaaaaataatlaaaatgtctcactgtgtgacatatttaattgattaag 1733
OY 1501 TACAGATGATTTTAACGTGTCACCTTTGTAATTCCTCTGAAGGCTACTCGTAGTAAGGG 1560
Db 1734 taacagatattttaactgtgcacttgttaattccctgaaaggtactcgtagctaaagg 1793
OY 1561 GCAGAAATACGTGTTCTGTGACACACATGATGTTATTTCTTTATCTTTAACTTAATA 1620
Db 1794 gcagaataactgtttctgtgtgacacatgtatgttattcttattcttattcctaata 1853
OY 1621 GAGTCTTCAG 1630
Db 1854 gagtcttcag 1863

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RESULT

8

ID AAV41489 standard; cDNA; 2191 BP.

AC AAV41489;

DT 24-SEP-1998 (first entry)

DE Nucleotide sequence of mouse 499E9 gene.

KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;

KW antagonist; autoimmune disorder; rheumatoid arthritis;

KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;

KW acute inflammatory response; antibody; antigen; cancer; ss.

OS Mus sp.

FH Key Location/Qualifiers

FT CDS 125..1072

FT FT /tag= a

FT FT /product= "mouse 499E9 protein"

PR 13-DEC-1996; 96US-0032846.

PA (SCHE) SCHERING CORP.

PI Gorman DM, Mattson JD;

DR WPI: 1998-348452/30.

DR P-PSDB: AAW59654.

PT Mouse cell surface antigen, 499E9 protein - used to treat conditions

PS associated with abnormal physiology or development

PS Claim 4; Pages 8-11; 59pp; English.

This is the nucleotide sequence encoding the mouse 499E9 protein, used in the method of the invention to treat conditions associated with abnormal physiology or development. The 499E9 protein is expressed highly on polarised Th1 T cells, binding of 499E9 to its receptor may result in either immune cell expansion or apoptosis. Antagonists of 499E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as acute inflammatory responses in which T cell expansion, activation or immunological T-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful

CC In detecting or diagnosing various (immunological) conditions related to
 CC the expression of antigens of 499p9. The antibodies, and fragments of
 CC 499p9 can be used in the treatment of conditions associated with
 CC abnormal physiology or development, including abnormal proliferation
 CC (e.g. cancerous conditions) or degenerative conditions.
 XX
 XX Sequence 2191 BP: 605 A: 461 C: 518 G: 607 T: 0 other:

Query Match 99.1%; Score 1615.8; DB 19; Length 2191;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CCGGGCTCCACAGAGGGTCCGTCACACCCGCGCTTCTGACACGGCTCCGGCCGC 60
 Db 189 ccgagccccaacagaggtccgcgcacccgcgccttcgcacgcgtccgcgcgcgc 248
 QY 61 CACCGCGCGCCCTCCGCTCCATGTTCTGCGCTCTCTGGGCTGGAGCTGGCCAGTGG 120
 Db 249 caccgcgcgcctccgcctccatgctccgcgcctccgcgcgcgcgcgcgcgcgcgcgc 308
 QY 121 TCTGCAGCATGCTCTGCT 180
 Db 309 tctgcagatagct 368
 QY 181 AAGACAGCATCTGCTCTTTTATAGATCTGAGACTCCATGAAACGACAGATTGACAG 240
 Db 369 aagacagacatcactcctcttataagaacltcgagactccatgaaacgcagcttcgacg 428
 QY 241 ACTGCAGCTGTGAGAGTGAAGACACATACCTGACTCTCTGAGAGAGATGAACAGCTT 300
 Db 429 actgcagctgtgagagtgagaaacacacactgactcctgagagagtgagaaacagctt 488
 QY 301 TTCAGGGGCGGTGAGAGAGTGAACATGATGTTGGGCGCACAGCGCTTCTCAGAG 360
 Db 489 ttcaggggcccgtgagagagagacacacacatctgaggccacagcgctctccagag 548
 QY 361 CTCGAGTATATGAGAGGCTCATGTTGGATGTGGCCACGAGAGCAAGCTTACAGGCC 420
 Db 549 ctccagctatgagtgagagagctcatggtgagtggtgcccagagagagagagagagcc 608
 QY 421 AGCCATTTGCACACCTTCACATCAATGCTGCAGATCCCTCGGGTTCCGATTAAGCA 480
 Db 609 agccatctgcac 668
 QY 481 CTCTGCTCTCTGTTGACACAGATGAGGCTGGCCAAAGATCTTACATGACGTTAAGCA 540
 Db 669 ctctgctctctctggttacacagatcgaagctgagccaaagatcttacaatgagctaa 728
 QY 541 ACGGAAACTAAGGGTTAACCAGATGGCTTCTATACCTGTACGCCAATTTGCTTTC 600
 Db 729 acggaaactaagggtttaaccagatggcttctataccttacctgacacacacacacacac 788
 QY 601 GGCATCATGAACATCGGAGAGCTTACCTACAGACTATCTTACGATGGTGTATGTCG 660
 Db 789 ggcatactgaaacatcggagagcgctacacagactatcttcagctgagtgtatctcg 848
 QY 661 TTAACACAGCATATAAATCCCAAGTTCTCATTAACGTATGAAGAGAGAGACAGAAAA 720
 Db 849 ttaaacacagcatataaattcccaagttctcataacccgatagaagagagagagagagaa 908
 QY 721 ACTGTCGGGCAATTTCGAATTCACCTTTATTCATAATGTTGGGGATTTTTCAGC 780
 Db 909 actgtcgggcaatttcgaatttcaccttttataataaagtgtgggagatttttcaagc 968
 QY 781 TCCGAGCTGTGAAGAAATTAAGATTCAAGTGTCAACACCTTCCCTCTGATCCGATC 840
 Db 969 tcgagctgtgtgaagaaatttaagattcaagtggttccaaaccttccctctgagatccg 1028
 QY 841 AAGATCGGAGCTACTTTGGGGCTTCAAAAGTTCAGCATAGACTGAGACTATTTCTGTG 900
 Db 1029 aagatcgagctacttttggggcttcaaaagtctcagagcatagactgagactatctctg 1088

QY 901 GAACATTAGCATGATGCTCTAGATGTTTGAACCTTCTTAAAAATGATGATGCTAT 960
 Db 1089 gaacattagcatgattgctctagatgtttgaaccttcttaaaaatgatgatgctat 1148
 QY 961 ACATGTGTAGACTACTAAGAGACATGGCCACGCTGTATGAACCTCAACAGCCCTCTCTC 1020
 Db 1149 acatgtgtagactactaagagacatggccacgctgtatgaacctcaacagccctctctc 1208
 QY 1021 TTGAGCCGTGACAGGTGTGTATATGTAAGTCCATAGCGATGTTGATTCATGAT 1080
 Db 1209 ttgagccgtgacaggtgtgtatatagtaaagttccatagcgatgttgatctcatg 1268
 QY 1081 TACACACGCGTTTACATTTTGAATGATTTCTT-GAATTTGACAGATTTGGAGAGG 1139
 Db 1269 tacacacgcgcttaccttcttgaatgatttcttgaatgatttggagagg 1328
 QY 1140 TATTCCGATGCTTATGAAAACTTACAGCTGAGCTATGGAAGGGGTACAGTCTCGGG 1199
 Db 1329 tattccgatgcttattgaaaaacttacagctgagctatggagggtacagtctcggg 1388
 QY 1200 TCTAACCCCTGAGATGTCGCCACTGAGAACCTTGAATTAAGAGATGCCATGTCTGC 1259
 Db 1389 tctaacccctgagatgtgccactgagaaaccttgaattaaagagatgccatgtctgc 1448
 QY 1260 AAGAAATGATAGTGTGAAGGGTTAAGTCTTTGAATTTGATTTGCGTGGAGCTG 1319
 Db 1449 aagaaatgatagtgtgaagggttaagcttttgaatttgaatttgcgtggagctg 1508
 QY 1320 CAATTAAGTCTTTTCTTATGAGAGAGAAAAATATATGATTTTATATATGCTCT 1379
 Db 1509 caatlaagctcttcttcttcaatgagagagaaaaataatgatttataatgctc 1568
 QY 1380 AAATGATATTTTACAGGTATGTTTCTGTCGCAAACTTTTGTAAATTAATTTGTGCTA 1439
 Db 1569 aaatgatttcttcttcttcaatgagagagaaaaataatgatttataatgctc 1628
 QY 1440 TAGTATTGATTCAAAATATTTAAAAATGCTCAGTGTGACATTAATTAATTTAAAT 1499
 Db 1629 tagtattgattctaaaatattttaaataatgctcagtggtgacatttaatttaatt 1688
 QY 1500 GTACAGATGATTTTAACTGCTGACCTTTGTAATTTCCCTGAAGTACTGATCCTAAGG 1559
 Db 1689 gtacagatgattttaaactgctgacctttgtaatttccctgaagctgactgactaagg 1748
 QY 1560 GGCAGATACCTGTTTGGGAGCACATGTAGTTTATTTCTTATCTTTTAACTTAAT 1619
 Db 1749 ggcagatacctgttctgggagcacatgtagtttattttcttattcttattcttaact 1808
 QY 1620 AGAGCTTTCAG 1630
 Db 1809 agagcttctcag 1819

RESULT 9
 AAX80224 standard; cDNA; 2237 BP.
 ID AAX80224;
 AC AAX80224;
 XX
 XX
 DT 17-AUG-1999 (first entry)
 XX
 XX Murine TRANCE encoding cDNA.
 DE
 DE TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
 KW TNF-related activation induced cytokine; Immune response; cancer;
 KW autoimmune disease; HIV; hypersensitivity; allergen; ds.
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH 142..1092
 FT CDS
 FT /tag= a
 XX

PN WO9923865-A2.
XX
PD 17-JUN-1999.
XX
PF 14-DEC-1998; 98WO-US26486.
XX
PR 11-DEC-1998; 98US-0989479.
PR 12-DEC-1997; 97US-0989479.
PR 03-MAR-1998; 98US-0034099.
XX
XX
PA (UYRO) UNITV ROCKEFELLER.
XX
PI Choi Y, Josien R, Steinman R, Won B;
XX WPI: 1999-385609/32.
DR P-PSDB: AA117874.
XX
PT TNF like proteins for treating autoimmunity and cancer
XX
PS Claim 4; Fig 3; 164pp; English.

AA The present sequence encodes murine TNF-related activation induced
CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
CC variants, fragments, derivatives or analogues may be used as modulators
CC of immune response in a mammal comprising, antisense sequences to
CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
CC Agonists and antagonists of TRANCE, can be used to modulate immune
CC response by increasing or decreasing the life span of mature dendritic
CC cells and increasing or decreasing T cell activation. These techniques
CC are especially useful for treating immune system related conditions such
CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
CC The TRANCE polypeptides can be used to increase the viability of
CC dendritic cells in vivo or in vitro, especially when used in conjunction
CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
CC CD40L or TNF-alpha).
XX
SQ Sequence 2237 BP; 636 A; 470 C; 519 G; 612 T; 0 other;

| Query Match | Similarity | 97.4% | Score 1588.2 | DB 20 | Length 2237 |
|--------------|--------------|---|--------------|-------|-------------|
| Best Local | Similarity | 99.6% | Prod. No. 0 | | |
| Matches 1624 | Conservative | 0 | Mismatches | 3 | Indels |
| | | | | | Gaps |
| QY | 1 | CCGCGCTCCACACAGAGGGTCCGCTGCACCCCGCGCTTCTGCACCGGCTCCGCGCCG | 60 | | |
| | | | | | |
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| DB | 206 | ccggcgtccacacaaagagtcctgcgtgcaccccgagctcttcgacagctcccgcgccg | 265 | | |
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| QY | 61 | CACCCGCGGCTCCCGCTCCATGTTCCGAGCCCTCCGAGGCGCTGGAGATGGCGAGGTG | 120 | | |
| | | | | | |
| | | | | | |
| | | | | | |
| DB | 266 | caccgcgcgcctccgcgtcccalgttctctgcccctccggyggtctgagcttggccaagtg | 325 | | |
| | | | | | |
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| | | | | | |
| QY | 121 | TCGACAGCATCGCTCTGTCTCTGTACTTTGAGCGCAGATGATCTTAACGAAATATAG | 180 | | |
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| DB | 326 | tcctgcagcatcgctctgtctctgaccttcgagcgagatgtgactctcaacagaaataag | 385 | | |
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| | | | | | |
| QY | 181 | AAGACACACATCATGCTGTTTATATGAATCCGACACTGCATGAAACCAATTTGCAGG | 240 | | |
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| DB | 386 | aagacacacactcaactgcttttatatgaatcccgagactccatgaaacgcaggtttgcag | 445 | | |
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| | | | | | |
| QY | 241 | ACTCGACTCTGAGAGTGAAGACACACTACTCTCTGACAGAGATGAACAAGCT | 300 | | |
| | | | | | |
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| DB | 446 | actcgactctgagagatggaagacacactactctgactctctgagagagatgaaacaagct | 505 | | |
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| | | | | | |
| QY | 301 | TTTCAGGGGGCGCTGCAGAGAAGACATGCAACATATGTGGGGCCACAGAGCTTCTAGAG | 360 | | |
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| DB | 506 | ttcagggggccggtgcagaagaagactgcacaacatgttgggccacagcgcttctcagag | 565 | | |
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| | | | | | |
| QY | 361 | CTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCACGAGAGCAAGCTTAGGGCC | 420 | | |
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| | | | | | |
| | | | | | |
| DB | 566 | ctccagctatgatggaaggtccatcagtgtgtgagatggcccaagaggaagcctgagccc | 625 | | |
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| | | | | | |
| | | | | | |
| QY | 421 | AGCATTTGCACACCTCCACATCATGTGCGCAGATCCCATCGGGTTCCATTAAGTCA | 480 | | |
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|----|------|--|------|
| Db | 626 | agccattgcaacacctcaacatcaatgctgccgaagcatccatcggtgtcccatatga | 685 |
| Qy | 481 | CTCTATCCCTCTTTGGTATCACGATCGAGGCTGGGCCAGATCTTATACATGACGTTTAAACA | 540 |
| Db | 686 | ctctgtccctctgtgtaccacgaatcgaggtcggtcccaagatctctacaatgacgttaagca | 745 |
| Qy | 541 | ACGGAATACTAAGGTTTAACCAAGTGGCTTCTATTACTCTAGCGCCAAATTTGGCTTTC | 600 |
| Db | 746 | acggaataactaagggttaaccaaagtgtctctatctacgttgaacgaacatltgcttc | 805 |
| Qy | 601 | GGCATCATGAACATTCGGGAACGTACTACAGATATCTTACCTGATGCTGATATGTCG | 660 |
| Db | 806 | ggcatcatgaacaacatcggaagcgtacctacaagctatcttcaagctgtgtgtatgtcgt | 865 |
| Qy | 661 | TTAAAAACGACATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGACAGAAAA | 720 |
| Db | 866 | ttaaaaacgcgtccaataatcccaagttcttcaatcctgatgtgaaggaaggaacagaaaa | 925 |
| Qy | 721 | ACTGTCGGGGCAATTCTGATTTCCACTTTTATTCCATAAATGTTGGGGATTTTTCAAGC | 780 |
| Db | 926 | actgttcgggcgaatctcgtatctcaatttcaataaagtgtggggatlttccaagc | 985 |
| Qy | 781 | TCCGAGCTGGTGAAGAAATTTAGCATTCAGTGTCCAAACCCCTCCCTGGTGATCCGATC | 840 |
| Db | 986 | tccgaagctgtgtgaagaaataacatcgaagtgttccaacccctccgtcgtgtccggatc | 1045 |
| Qy | 841 | AAGATTCGACGATCTTTGGGGCTTTCAAAAGTTTCAGACATAGACTGACATCTTTCTGTG | 900 |
| Db | 1046 | aagatgtcgagctactcttgggtcttcaaaagttccaagacaatagacgtgagctacttctgt | 1105 |
| Qy | 901 | GAACATTTACATGAGATGTCCTTAGATGTTTGGAACTCTTAAATAAGATGATGCTAT | 960 |
| Db | 1106 | gaacatlaagatgagtgcttcctgaagtgttctggaacttcttaaaaaatgtgaatgtctct | 1165 |
| Qy | 961 | ACATGCTGTAGAATCTACTTAAGACATGAGCCGACGCTGTATGGAACATCACAGCCCTCTTC | 1020 |
| Db | 1166 | acatgtgtgaagactactaagaagacataggtccacgtgtatgtgaacatccacagccctcttc | 1225 |
| Qy | 1021 | TTGAG-CCTGTACAGGTTGTGTATATGTAAAGTCATAGGTGATGTTACATTCATGCTGA | 1079 |
| Db | 1226 | ttgagccctgtacaggtgtgtatagtatagtaaagtcataagtgatgtatgaattcatgttga | 1285 |
| Qy | 1080 | TTTACACACGCTTTACAAATTTTGTATATATTTCCTAGAATTGAACACAGATTGGGAGAG | 1139 |
| Db | 1286 | ttacacaacggttttcaatlttgaatgtatcttccagaatgtgaacgaatctgtggagaag | 1345 |
| Qy | 1140 | TATTCGATGCTTATGAAAACTTACACGAGACCTATGGAAGGGGTCTCAGTCTGTGG | 1199 |
| Db | 1346 | tattccgaatgtatgaaaaaacttacaacgtgagctatgtgaagggtgtccagctctc-99 | 1404 |
| Qy | 1200 | TCTAACCCCTCGACATGTGGCACTGAGAACCTTGAATTAAAGAGATGCCATGCTATTGC | 1259 |
| Db | 1405 | tctaacccctcgagacgtgtgcactgtgaaccttgaatlaaagtgatgcattgtcatgtgc | 1464 |
| Qy | 1260 | AAAAGAAATGATAGTGTGAAGGTTAACTTTTGTGAATGTTACATTTGGCTGGGACCTG | 1319 |
| Db | 1465 | atagaatgtatgtgtgaagggtlaagttcttcttgaatgttacaatltgcgtctgtggaccgt | 1524 |
| Qy | 1320 | CAAAATAGTCTTTTCTTATAGAGAGAGAAAAATATATGATTTTATATAAAGTCTA | 1379 |
| Db | 1525 | caaatagttcttcttcttccaagag--gagaaaaataatagtcatcttctataataatgtctc | 1582 |
| Qy | 1380 | AAATGATTAATTTGAGTGTATGTTTTCTGTGCAAAAGTTTGTAAATATATTTGTGCTA | 1439 |
| Db | 1583 | aaagtataattctgaagtgatagtttctctgtgcaaaagttctgtlaaatatataattgtgcta | 1642 |
| Qy | 1440 | TAGTATTTGATCAAAATATTTAAAAATGTCTACGTGTGACATATTATATGTTTTAAAT | 1499 |
| Db | 1643 | tagtatctgtatcaaaaatatttaaaaaatgtctacatgtgtacatatttaatgttcttaaat | 1702 |
| Qy | 1500 | GTAAGATGTAATTAACGTGGTGCCTTTGTAATTTCCCTGAAGGTACTCTAGCTAAGG | 1559 |
| Db | 1703 | gtlaaagatgtatccaacgtgtgaccttgttaattccctctgaaggtaactcgttaagtaagg | 1762 |

| | | | |
|---|----------------------------------|---|------|
| OY | 1560 | GGCGAATACGCTTTTCGCGACCAATGTAAGTTATTTCTTTTAACTTAAT | 1619 |
| DB | 1763 | ggcgaaatcgcgtttctcgtgcacacatgtagttatcttattctttaactaat | 1822 |
| OY | 1620 | AGAGCTTTCAG | 1630 |
| DB | 1823 | agagcttcacg | 1833 |
| RESULT | 10 | | |
| AAV6986 | | | |
| AAV6986 | standard; cDNA to mRNA; 1538 BP. | | |
| AAV6986; | | | |
| 10-FEB-1999 | (first entry) | | |
| Nucleic acid encoding an OCIF-binding molecule (OBM). | | | |
| Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism; | | | |
| 88. | | | |
| Unidentified. | | | |
| Key | Location/Qualifiers | | |
| CDS | 125..1075 | | |
| | /*tag= a | | |
| MO9846644-A1. | | | |
| 22-OCT-1998. | | | |
| 15-APR-1998; | 98MO-JP01728. | | |
| 02-DEC-1997; | 97JP-0332241. | | |
| 13-APR-1997; | 97JP-0097808. | | |
| 09-JUN-1997; | 97JP-0151434. | | |
| 12-AUG-1997; | 97JP-0217897. | | |
| 21-AUG-1997; | 97JP-0224803. | | |
| (SNOW) | SNOW BRAND MILK PROD CO LTD. | | |
| Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T; | | | |
| Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E; | | | |
| Mashida N, Yamaguchi K, Yano K, Yasuda H; | | | |
| WPI; 1998-594563/50. | | | |
| Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and calcium metabolism | | | |
| Claim 9; Pages 108-109; 151pp; Japanese. | | | |
| The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as components of drugs. | | | |
| Sequence 1538 BP; 382 A; 381 C; 416 G; 359 T; 0 other; | | | |

| Query Match | 82.74; | Score 1348.4; | DB 19; | Length 1538; |
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| Best Local Similarity | 99.94; | Pred. No.0; | Mismatches | 1; |
| Matches 1349; | Conservative | 0; | Indels | 0; |
| Gaps | | | | |
| QY | 1 | CCGGGGCTCCACACAGAGGTCGCGTGCACCCCGGCTTGTGACAGGGTCGCGGGCGGC | 60 | |
| DB | 189 | ccggggtccccaacagaggttcgcgtcaaccccgcccttcgcagcgctccggcgccgc | 248 | |
| QY | 61 | CACCCGCGCCTCCCGCTCATGTTCTCTGGCCCTCTCGGGGCTGGGACTCGGCAAGTGG | 120 | |
| DB | 249 | caaccgcgcctcccgctcccatgtctctggcccttcgggctcgggacatggcgccagtg | 308 | |
| QY | 121 | TCTGGAGCATGCGTCTGTTCTCTGTAATCTTGGAGCGCAGATGATCTCTAACAGATATCAG | 180 | |
| DB | 309 | tcctgacagatcgcctctgtctctgaactctcgagcgagagatgccctaaagaaatacag | 368 | |
| QY | 181 | AAGACAGCACTCACTGCTTTTATGAAATCCGTGAGACTGCATGAAACGCAAGATTGGCAGG | 240 | |
| DB | 369 | aagacagacatcacctgcctttatagaatcctctgagctccatgaaacgcaagtttgcag | 428 | |
| QY | 241 | ACTGCATCTGGAAGCTGAGACACTACCTGACTCTGACAGAGATGAACAAGCTT | 300 | |
| DB | 429 | actgcactctggagatgtaagacacactacactgactcctcgcaagagatgaaacaagcct | 488 | |
| QY | 301 | TTTCAGGGGCGGTGAGAGAAATGTCACACATTTGGGGGCGCACAGGCGCTTCTCAGAG | 360 | |
| DB | 489 | ttcagggggccgctgcagagaaacatgaaacacatcttggggccacacgctctccagag | 548 | |
| QY | 361 | CTCCAGTATGATGGAAGGCTCATGTTGGATGTGGCCACGAGGCAAGCCTTGAGGCC | 420 | |
| DB | 549 | ctccagcatatgataagagctcaatggttgaatgtggccagggcgaagccttgagcc | 608 | |
| QY | 421 | AGCCATTGSCACACCTCACCATCAATGCTGTCCAGCATCCGATCGGGTTTCCCAATAAGTCA | 480 | |
| DB | 609 | agccatttgcaacctcaacataatgctgcagacatcccatcgggtttcccaataagatca | 668 | |
| QY | 481 | CTCTGTCCCTTTGGTTACACAGATGAGAGCGCGGCGCAAGATCTCTAACATGAGCTTAACA | 540 | |
| DB | 669 | ctctgtcctcttggtaacacagatcgaggtgcgagacatcctcaatcatgacgttaagca | 728 | |
| QY | 541 | ACGGAANAATTAAGGTTTACCACAGATGCGTTCTATTACCTGTACGGCAACATTTGCTTTC | 600 | |
| DB | 729 | acggaanaactaaggtttaacaaagatgctctctatcactgtaagccaacattctcttc | 788 | |
| QY | 601 | GGCATCATGAACAATCGGGAAGGTAACCTCAACATCTGACGCGATGCTATGTCG | 660 | |
| DB | 789 | ggcatcatgaaacatcggggaagcgttaacctcaagaacatcctcagctgagtgatgtc | 848 | |
| QY | 661 | TTTAAACCAAGCATCAAAATCCCAAGTTCTCATTAACCTGTATGANAAGAGAGACACAGANA | 720 | |
| DB | 849 | tttaaacacagatcaaaaatcccaagtctctcaatacctgtgaaaggggagcagagaaa | 908 | |
| QY | 721 | ACTGTCGGGCAATTTCTGAAATTCACATTTTATTCATAAATGTTGGGGATTTTTCAGC | 780 | |
| DB | 909 | actgtctgggaattctgtaattccactcttatccataaaatgttggggatatttccaagc | 968 | |
| QY | 781 | TCCGAGTGGTGAAGAATTAAGATTACATTACAGTGTGCACAACTTCCCGCGGATTCGGATC | 840 | |
| DB | 969 | tcggagctggggaagaataatgacatccaggtgtccaacccctccctgtgtatccggatc | 1028 | |
| QY | 841 | AAGATGCAGCTACTTTTGGGCTTTTCANAAGTTTCAGGACATTAAGTACATCATTTTCGTG | 900 | |
| DB | 1029 | aagatgcagactactcttgggcttccaagttccaggaacatgagacgtgacatcaatttcg | 1088 | |
| QY | 901 | GAACATTATAGATGGATGCTCTAGATGTTTGGAAACCTTTTAAAAAATGAGATGATGTAT | 960 | |
| DB | 1089 | gaacctatgacttggatgtccctagatgtcttggaacctctttaaaaaatgatatgtctat | 1148 | |
| QY | 961 | ACATGTGTAAAGACTACTTAAGACATGAGGCCACAGGATGTGAAGATCAACAGCCCTCTTC | 1020 | |
| DB | 1149 | acatgtgttaagaaactaaataaagatagggccagagatgtatgaaatcttgcacccctcttc | 1208 | |

| | | | |
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| Dd | 1118 | atcatattctgctcgtacgtatcttgattgcataaaattcaaaaatcgctccaccgttcgacata | 1177 |
| Oy | 1485 | TTTTAATGTTTTTAAATGTACAGATGTATTTTAACTGGTGACATTGTGAATTCCTGAAGGT | 1544 |
| Dd | 1178 | tttaaatgcttctaabaatgtaacagatgatatttaaacatggtgacctgg-aattccccgaagt | 1236 |
| Oy | 1545 | ACTCGTAGCTTAAGGGGGCAGAATPACTGTTTCCGCGACCACATGATGATTATTTCTTAT | 1604 |
| Dd | 1237 | actcgttagcttaaaggaggaacacgtcttcctgvtgacacaatgatttatctctat | 1296 |
| Oy | 1605 | TCTTTTAACTTAATAGAGCTTTCAG | 1630 |
| Dd | 1297 | tctttaacttaataagatgcttcag | 1322 |
| RESULT | 12 | | |
| AAZ99964 | ID | AAZ99964 standard: DNA; 2271 BP. | |
| XX | AC | AAZ99964; | |
| XX | DT | 25-JUL-2000 (first entry) | |
| XX | DE | DNA encoding a human osteoprotegerin ligand (OPGL). | |
| XX | KW | Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; | |
| XX | KM | tumour necrosis factor receptor type II transmembrane protein; | |
| XX | KW | osteoclast differentiation; CSF-1; osteoclast activator; | |
| XX | OS | immune response; osteoporosis; bone resorption; ss. | |
| XX | FM | Homo sapiens. | |
| XX | FT | Key Location/Qualifiers | |
| XX | CDS | 185..1138 | |
| XX | FT | /tag= a | |
| XX | FT | /product= "osteoprotegerin ligand" | |
| XX | PM | WO200015807-A1. | |
| XX | PD | 23-MAR-2000. | |
| XX | PF | 13-SEP-1999; 99WO-DK00481. | |
| XX | PR | 15-SEP-1998; 98DK-0001164. | |
| XX | RR | 02-OCT-1998; 98US-0102896. | |
| XX | PA | (MEBI-) M & E BIOTECH AS. | |
| XX | PI | Haikler T, Henning J; | |
| XX | DR | WPI: 2000-271444/23. | |
| XX | P | P-PDB: AAY84417. | |
| XX | PS | In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used | |
| XX | PS | to treat, prevent and ameliorate osteoporosis - | |
| XX | XX | Disclosure: Page 75-77; 110pp; English. | |
| CC | XX | The present sequence encodes a human osteoprotegerin ligand (OPGL). | |
| CC | XX | Osteoprotegerin is a secreted member of the tumour necrosis factor | |
| CC | XX | receptor family, which blocks osteoclastogenesis in a dose dependent | |
| CC | XX | manner. The OpGL protein is synthesized as a type II transmembrane | |
| CC | XX | protein. The murine and human OPGL polypeptides are 87% homologous. OPGL | |
| CC | XX | is a potent osteoclast differentiation factor when combined with CSF-1. | |
| CC | XX | It is not capable of inducing osteoclast differentiation in the absence | |
| CC | XX | of CSF-1. OPGL is also an activator of mature osteoclasts. The | |
| CC | XX | specification describes a method for the in vivo down-regulation of | |
| CC | XX | OPGL activity in an animal. The method comprises using at least one OPGL | |
| CC | XX | polypeptide or subsequence, and/or at least one OPGL analogue to induce | |
| CC | XX | an immune response in the animal. The method and OPGL polypeptide are | |
| CC | XX | useful for treating, preventing and ameliorating osteoporosis or other | |
| CC | XX | diseases or conditions characterised by excessive bone resorption. | |

[illegible]


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Db 606 gtagcagagaaacgtagtgcgtacgtgttagatcttgccagaagagagcgttg 665
Oy 415 AGCCAGACCAATTTGCACACCTCACCATCAATGCTGCCAGATCCCATCGGTTCCATA 474
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Db 666 aagctcagcccttctgctcactcactatlaagtcacacgcaatcccatctgttccata 725
Oy 475 AAGTCACTGTGCTCTTGTGTACACGATCGAGGCTGGCCAAAGATCTCTAATCATGAGCT 534
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 726 aagtagtctgtccctctgtgtacccaatgacggtctggcacaagatctccaacatgact 785
Oy 535 TAAGCAACGGAACGTAAGGTTTAACCAAGATGCTTCAATACGTTACGTCACCAATTT 594
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Db 786 ttagcacaagaaactaaactaagtaactcaagacggtcttattatccatgacacatct 845
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Db 846 gcttctgacatcatgaacttcagagaccttagctacagagatcttcaactaaagtgct 905
Oy 655 ATGTGCTTAAACACGACATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGCA 714
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Oy 715 CGAAAAACGTGGCGCAATTTGTAATTCGACTTTTATTCATTAATGTTGGGGATTTT 774
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Db 966 ccaagtatctgcaaggaatctcgaatccatttcaatccataaagcttggtgagatct 1025
Oy 775 TCAAGCTCCGAGCTGCTGTAAGAAATTAAGCATTCAGGTGCCAACCCTTCCCTGCTGATC 834
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Db 1026 ttaagtlacggtctgagagagaaatcagcatcgaggtccaaacccctctacagatc 1085
Oy 835 CGGATCAAGATGCGACGACTTGTGGGCTTCAAAAGTTCAGACACTATGACTGAGACTAT 894
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Db 1086 cggatcagagatgcaacatactctggggtctttaaagttcagatataagatgagccag 1145
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Db 1146 tcttcggagtgct---atgattcttcgtgagtgcttggaacatctttaaacaagccaa 1202
Oy 948 GGATGATGCTTAATACATGCTGAAGACTACTAAGACATGCCCCAGGCTGATGAAGCTC 1007
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Db 1203 gaaagatgatatagtgctgtagactactaagagacatgagcccaagagcaagactc 1262
Oy 1008 ACAGCCCTCTCTTGAGCCCTGTACAGTGTGCTATATGTAAGTCCATAGTATGATTTA 1067
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Db 1263 agtaccctctgctcgtacgtctgtagaacaacgctatccaagcagtgagagtgta 1322
Oy 1068 GATTGATGCTG-ATTACACAACGGGTTTACAATTTGTAAGATTTCTAGAAATGAGACC 1126
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Db 1323 gactcaatgctgttacaacaatggtcttcaaatcttcaatgaatctcctaagaattaaac 1382
Oy 1127 AGATTGGAGAGGTAATTCGATGCTTATGAAMAACTACAGCTGAGTATGGAAGGGGT 1186
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Oy 1427 TATATTTGCTATATGATTTGATTCAAAAATTTAAAAATGCTCACTGTTGACATATT 1486
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Db 1721 taagtlttaaatgtaacagacataatctacgtgacatcttgtaaatcccttggggaaba 1780
Oy 1542 GGTACTGCTAGCTAAGGGGAGAAATTAAGTCTTGTGTGACCACTAGTATTTTCTT 1601
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RESULT 14
AAV69900
ID AAV69900 standard; cDNA to mRNA; 951 BP.
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XX AAV69900;
XX
XX 10-FEB-1999 (first entry)
XX
XX Nucleotide sequence of the specification.
XX
XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
XX osteoclast; bone absorption factor; bone disorder; calcium metabolism;
XX ss.
XX Unidentified.
XX
XX M09846644-A1.
XX
XX 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-JP01728.
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XX 02-DEC-1997; 97JP-0332241.
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XX 15-APR-1997; 97JP-0097808.
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XX 09-JUN-1997; 97JP-0151434.
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XX 12-AUG-1997; 97JP-0217897.
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XX 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
XX Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
XX Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI: 1998-594563/50.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
XX for, e.g. treatment and investigation of disorders of bone and
XX calcium metabolism
XX
XX Disclosure; Pages 116-117; 151pp; Japanese.
XX
XX The present sequence appears in the specification, which describes
XX an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
XX The protein promotes and supports the separation and maturation of
XX osteoclasts in the presence of bone absorption factors such as
XX calcitriol or parathyroid hormone (PTH). OBM is isolated from
XX stroma cells cultured in the presence of a bone absorption factor
XX by separation and solubilisation of membrane proteins then affinity
XX chromatography using OCIF. It exists in a full-sequence form and a
XX solubilised form (SOBM) which is a shorter chain. OBM may be used
XX for screening potential inhibitors and modifiers of its biological
XX activity, and screening for receptors to OBM which mediate its function.
XX These substances can then be used in the treatment of disorders of bone
XX function and calcium metabolism. The antibodies can be used for assay
XX of the protein, for investigative and diagnostic purposes, and as
XX components of drugs.
XX
XX Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;
XX

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Query Match 54.3%; Score 885.4; DB 19; Length 951;
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 Matches 886; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 61 CACCCGCGCCCTCCCGCTCATGTTCTCGGCCCTCCTGGGCGTGGAGTGGCCAGGTGG 120
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Db 125 caccgcgcgctccgcgcctcatgttcctcgccctccctcgggctggaactggccaagtg 184
OY 121 TCTGCAGCATGCTCTGTTCTCTGACTTTCGAGCGGAGATGGATGCTTAACGAATATCAG 180
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Db 185 tctgcagcatgctctgtctctgtactcttcgagcgcaagtgtctcctaacaagatatac 244
OY 181 AAGACAGCACTACATGCTTTATAGATCTGAGACTCCATGAAAACGAGATTTCAGG 240
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Db 545 cctgtgctcttgataccagatcgagtcgagtcgagtcgagtccttaacatgagcttaaga 604
OY 541 ACGGAAAATAAGGTTAAACAAGATGGCTTCTATTACCTGTGACGCCAACATTTGCTTTC 600
    |||
Db 605 acggaaaataagggtttaaacaagatggcttctattacctgtaacgcaacattgcttc 664
OY 601 GGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTACGCTGATGGTATATGCG 660
    |||
Db 665 ggcatactgaacaatcgggaagcgtaacctacagactatcttcaagctgagtgatgctg 724
OY 661 TTTAAACCGCAGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAAGGAGGAGCA 720
    |||
Db 725 ttaaacccgagcatcaaaatcccaagttctcataaactgttgaaagagaggaacagaaaa 784
OY 721 ACTGTCGGGCAATTCCTGATTCACATTTTATTCATTAATGTTGGGGAATTTTCAACG 780
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Db 785 actgtcgggcaattccttgatcttaccactttatccaataatgttggggaattttcaagc 844
OY 781 TCCGAGCTGTGAAGAAATTTAGCATTCAGGTGTCGAACCTTCCCTGCTGATCCGAGTC 840
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Db 845 tccgagctgttgaaagaataatagcatcagtggtccaaccttccctcgttgatccgagtc 904
OY 841 AAGACGAGCACTACTGCTTTTATAGATCTGAGACTCCATGAAAACGAGATTTCAGG 887
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Db 905 aagacgagcactactgctttatagaaacctcgagactccaagaaacgagtttcagag 951
  
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DT 05-SEP-2000 (first entry)
 XX Mouse OBM nucleotide sequence SEQ ID NO:9.
 DE Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF;
 XX Mouse; osteoclast; Bone absorption promoting factor; vitamin D3; PTH;
 KW OBM; osteoclast; Bone absorption promoting factor; vitamin D3; PTH;
 KM parathyroid hormone; ds.
 XX Mus sp.
 OS Mus sp.
 PN JF2000102390-A.
 XX 11-APR-2000.
 PD 11-APR-2000.
 XX 30-SEP-1998; 98JP-0292971.
 PE 30-SEP-1998; 98JP-0292971.
 PF 30-SEP-1998; 98JP-0292971.
 PR 30-SEP-1998; 98JP-0292971.
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX (YSNE-) YS NEW TECHNOLOGY KENKYUSHO.
 PA WPI: 2000-332087/29.
 DR P-PSDB: AAY91024.
 DR A DNA and preparation of a protein by using it -
 XX Example 1; Page 15; 18pp; Japanese.

XX The present invention describes a genomic DNA encoding a protein having
 CC an activity of supporting or promoting differentiation and maturation of
 CC osteoclasts. The genomic DNA encoding a protein has the following
 CC properties: (a) combines specifically with osteoclastogenesis inhibitory
 CC factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)
 CC of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide
 CC gel electrophoresis) under a nonreductive condition and the apparent mw
 CC when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c)
 CC has an activity of supporting or promoting differentiation and maturation
 CC of osteoclast in the co-culture of mouse osteoblast-like stroma cell and
 CC mouse spleen cell in the presence of a bone absorption promoting factor
 CC such as active type vitamin D3 and parathyroid hormone (PTH). The protein
 CC can be used as a drug and a research reagent. The present sequence
 CC encodes a mouse OCIF binding molecule (OBM) from the present invention.

XX Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other:
 SQ

Query Match 54.3%; Score 885.4; DB 21; Length 951;
 Best Local Similarity 99.9%; Pred. No. 2.8e-223;
 Matches 886; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 CCGGCGTCCACAGAGGAGTCCGTCGACCCCGGCGCTTTCGACCGGCTCCGGCGCGC 60
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OY 61 CACCCGCGCCCTCCCGCTCATGTTCTCGGCCCTCCTGGGCGTGGAGTGGCCAGGTGG 120
    |||
Db 125 caccgcgcgctccgcgcctcatgttcctcgccctccctcgggctggaactggccaagtg 184
OY 121 TCTGCAGCATGCTCTGTTCTCTGACTTTCGAGCGGAGATGGATGCTTAACGAATATCAG 180
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Db 185 tctgcagcatgctctgtctctgtactcttcgagcgcaagtgtctcctaacaagatatac 244
OY 181 AAGACAGCACTACATGCTTTTATAGATCTGAGACTCCATGAAAACGAGATTTCAGG 240
    |||
Db 245 aagacagcactacatgctttatagaaacctcgagactccaagaaacgagtttcagag 304
OY 241 ACTGCAGTCTGGAGATGAAGACACACTACTGACTCCTCGAGAGAGATGAACAAGCCT 300
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Db 305 actgcagctctggagagtgagaaacacactaccctcgagactccaagaaacgagtttcgacg 364
OY 301 TTCAGGGGGCGCTGCAGAAAGACTGCAACACATTTGTGGGGCCACAGGCTTCTCAGGAG 360
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Db 365 ttcagggggcgctgcagaaagactgcaaacacatgtgaggggccacagagctctcagag 424
  
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| | | | |
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| OY | 361 | CTCCAGCATATGATGGAAGGCTCATGTGGATTGTGGCCCAAGGAGGCGAAGCCTGAGGCC | 420 |
| Db | 425 | CTCCAGCATATGATGGAAGGCTCATGTGTGATGTGGCCCAAGGAGGCGAAGCCTGAGGCC | 484 |
| OY | 421 | AGCCATTTTGCAACACTCAGCATCAATGCTGGCAGACATCCCATCGGGTTCCTATAAGTCA | 480 |
| Db | 485 | agccatcttgcaaacctcagcatcaaatgctgtgcagcagcccatcgggtttcccaataagctca | 544 |
| OY | 481 | CTCTCTCTCTTTGGTACACAGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTAAGA | 540 |
| Db | 545 | ctctctctcttggtaacacagatctgaagctgtggcacaagactctcaacatgaagctaaagca | 604 |
| OY | 541 | ACGGAAAACTAAGGTTTAACCAATGAGTTCCTTTACTCTGTACGGCAACATTTGGTTTC | 600 |
| Db | 605 | acggaanaactaagggttaacacagaigtctctcatatccctcagtaagccaaattcgcttctc | 664 |
| OY | 601 | GGCATCATGAACATTCGGGAAAGGCTACCTACAGACTATCTTCAGCTGATGTTATGTG | 660 |
| Db | 665 | ggcatcatgaaacctcgggaagcttacctcagactatcttcacgcgtaagtggtatgctg | 724 |
| OY | 661 | TTTAAACACGACATCAAAATCCCAAGTTCTCATTAACGATGAAGAAGAGAGACCAAAA | 720 |
| Db | 725 | ttaaacacagatcatcaaaatcccaagttctcataactgtaagaagaaggagacagaaaa | 784 |
| OY | 721 | ACTGATGGGCAATTCGATTTCACATTTTATTCATTAATGTTGGGGCATTTTTCAAAC | 780 |
| Db | 785 | actgctcggaatacttcgaaatcccaacttattcctaataagtttggggatatttccaagc | 844 |
| OY | 781 | TTCGAGCTGTGTAAGAAATTAGCATTCAGGTGTCAAACTTCCCTGCGGATTCGGGATC | 840 |
| Db | 845 | tccgagctgtgtgaagaattatgattccaggtgtgccaaaccttcacctgcgtgattccggtatc | 904 |
| OY | 841 | AAGTATCGAGCATCTATTGGGGGCTTCAAGATTACAGACATAGACTGA 887 | |
| Db | 905 | aagatgtgacgtactctcttggggcttccaagaattcaagatactaacctga 951 | |

Search completed: July 8, 2002, 21:43:41
Job time: 6075 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 19:52:41 ; Search time 96.15 Seconds
(without alignments)
4164.146 Million cell updates/sec

Title: US-09-865-363-10

Perfect score: 1630
Sequence: 1 CCGCGCTCCACACGAGGCT.....TAAGTTATAGAGTCTTCAG 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1na/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 1630 | 100.0 | 1630 | 3 US-08-996-139-10 | Sequence 10, App1 |
| 2 | 1630 | 100.0 | 1630 | 4 US-08-995-659-10 | Sequence 10, App1 |
| 3 | 1630 | 100.0 | 1630 | 4 US-09-215-649A-10 | Sequence 10, App1 |
| 4 | 1628.4 | 99.9 | 2295 | 2 US-08-842-842-6 | Sequence 6, App1 |
| 5 | 1628.4 | 99.9 | 2295 | 4 US-09-052-521C-1 | Sequence 1, App1 |
| 6 | 1615.8 | 99.1 | 2191 | 4 US-08-989-362-1 | Sequence 1, App1 |
| 7 | 939.6 | 57.6 | 2271 | 4 US-09-052-521C-3 | Sequence 3, App1 |
| 8 | 615 | 37.7 | 954 | 3 US-08-996-139-12 | Sequence 12, App1 |
| 9 | 615 | 37.7 | 954 | 4 US-08-995-659-12 | Sequence 12, App1 |
| 10 | 615 | 37.7 | 954 | 4 US-09-215-649A-12 | Sequence 12, App1 |
| 11 | 58.4 | 3.6 | 759 | 4 US-09-320-424-10 | Sequence 10, App1 |
| 12 | 58.4 | 3.6 | 768 | 4 US-09-320-424-12 | Sequence 12, App1 |
| 13 | 58.4 | 3.6 | 1042 | 3 US-08-584-031-2 | Sequence 2, App1 |
| 14 | 58.4 | 3.6 | 1042 | 3 US-08-780-496-2 | Sequence 2, App1 |
| 15 | 58.4 | 3.6 | 1521 | 1 US-08-670-354-3 | Sequence 3, App1 |
| 16 | 58.4 | 3.6 | 1521 | 4 US-09-320-424-3 | Sequence 3, App1 |
| 17 | 58.4 | 3.6 | 1521 | 5 PCT-US96-10895-3 | Sequence 3, App1 |
| 18 | 58.4 | 3.6 | 1751 | 1 US-08-670-354-1 | Sequence 1, App1 |
| 19 | 58.4 | 3.6 | 1751 | 4 US-09-320-424-1 | Sequence 1, App1 |
| 20 | 58.4 | 3.6 | 1751 | 5 PCT-US96-10895-1 | Sequence 1, App1 |
| 21 | 58.4 | 3.6 | 1769 | 4 US-09-333-593A-5 | Sequence 5, App1 |
| 22 | 58.4 | 3.6 | 1769 | 4 US-09-505-250-1 | Sequence 5, App1 |
| 23 | 58.4 | 3.6 | 1366 | 1 US-08-670-354-5 | Sequence 5, App1 |
| 24 | 54 | 3.3 | 1366 | 4 US-09-320-424-5 | Sequence 5, App1 |
| 25 | 54 | 3.3 | 1366 | 5 PCT-US96-10895-5 | Sequence 5, App1 |
| 26 | 46 | 2.8 | 5526 | 3 US-08-751-359-21 | Sequence 21, App1 |
| 27 | 46 | 2.8 | 5526 | 4 US-08-907-146-21 | Sequence 21, App1 |

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| C | 28 | 45.2 | 2.8 | 688 | 4 | US-08-998-416-972 | Sequence 972, App |
| | 29 | 45 | 2.8 | 662 | 4 | US-08-998-416-185 | Sequence 185, App |
| | 30 | 45 | 2.8 | 665 | 4 | US-08-998-416-937 | Sequence 937, App |
| | 31 | 45 | 2.8 | 701 | 4 | US-08-998-416-701 | Sequence 701, App |
| | 32 | 45 | 2.8 | 724 | 4 | US-08-998-416-683 | Sequence 683, App |
| | 33 | 45 | 2.8 | 732 | 4 | US-08-998-416-1036 | Sequence 1036, App |
| | 34 | 45 | 2.8 | 767 | 4 | US-08-998-416-472 | Sequence 472, App |
| | 35 | 45 | 2.8 | 827 | 4 | US-08-998-416-535 | Sequence 535, App |
| | 36 | 45 | 2.8 | 828 | 4 | US-08-998-416-538 | Sequence 538, App |
| | 37 | 45 | 2.8 | 834 | 4 | US-08-998-416-305 | Sequence 305, App |
| | 38 | 44.8 | 2.7 | 711 | 4 | US-08-998-416-786 | Sequence 786, App |
| | 39 | 44.2 | 2.7 | 6132 | 4 | US-08-973-462-1 | Sequence 1, App1 |
| | 40 | 43.4 | 2.7 | 6243 | 2 | US-09-056-075-1 | Sequence 1, App1 |
| C | 41 | 43.2 | 2.7 | 19124 | 2 | US-08-487-8268-13 | Sequence 13, App1 |
| | 42 | 42.2 | 2.6 | 782 | 4 | US-08-998-416-224 | Sequence 224, App |
| | 43 | 41.6 | 2.6 | 6124 | 4 | US-08-213-4198-3 | Sequence 3, App1 |
| | 44 | 41.4 | 2.5 | 1826 | 4 | US-09-286-691-11 | Sequence 11, App1 |
| C | 45 | 41.4 | 2.5 | 1826 | 4 | US-09-687-147-11 | Sequence 11, App1 |

ALIGNMENTS

RESULT 1
US-08-996-139-10
; Sequence 10, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1630 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

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:      ANTI-SENSE:  NO
:      ORIGINAL SOURCE:
:      ORGANISM:  Mus musculus
:      IMMEDIATE SOURCE:
:      LIBRARY:
:      CLONE:  RANRL
:      FEATURE:
:      NAME/KEY:  CDS
:      LOCATION:  3..884
:      US-08-996-139-10

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| Query Match | Similarity | 100.0% | Score 1630: | DB 3: | Length 1630: |
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| Best Local | Similarity | 100.0% | Pred. No. 0: | | |
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| Db | 1 | CCGGGCTCCCAACACAGAGGGTCCGCTGACACCCCGCGCTTCTGACACCGAGCTCCGGCGCCG | 60 | | |
| QY | 61 | CACCCGCCGCCCTCCGCTCCATGTTCTGTGGCCCTCTCTGGGGCTGGGACTGGGCCAGGTGG | 120 | | |
| Db | 61 | CACCCGCCGCCCTCCGCTCCATGTTCTGTGGCCCTCTCTGGGGCTGGGAGTGGGCCAGGTGG | 120 | | |
| QY | 121 | TCTGACAGACTGCGCTCTGTCTTCCTGCTACTTTCGAGCGGACGAGATGGATCTCTAACAGAAATFCA | 180 | | |
| Db | 121 | TCTGACAGACTGCGCTCTGTCTTCCTGCTACTTTCGAGCGGACGAGATGGATCTCTAACAGAAATFCA | 180 | | |
| QY | 181 | AAGACAGCACTACTGCTTTTATAGAACTCTAGACTCCATGCAAAACGAGATTTTCAG | 240 | | |
| Db | 181 | AAGACAGCACTACTGCTTTTATAGAACTCTAGACTCCATGCAAAACGAGATTTTCAG | 240 | | |
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| Db | 241 | ACTCGACTCTGAGAGTGAAGACACACTACTGCTGCTGCTGACGAGAGATGAACAAAGCCT | 300 | | |
| QY | 301 | TTTCAGGGGGCCCGCGAGGAAGAACTGCAACACATTTGGGGGCCACAGCGCTTCTCAAG | 360 | | |
| Db | 301 | TTTCAGGGGGCCCGCGAGGAAGAACTGCAACACATTTGGGGGCCACAGCGCTTCTCAAG | 360 | | |
| QY | 361 | CTCCAGACTATGATGAAGGCTCATGTGTTGATGTGGCCCGCAGCGAGCCAAAGCCTGAGGCC | 420 | | |
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| Db | 421 | AGCCATTTGACACCTCCACCATCATGTCTGACAGATCCCATGGGTTCCCATTAAGTCA | 480 | | |
| QY | 481 | CTCTGCTCTTGTGTACACAGATCGAGGGGGGCCAAAGATCTTAACATGACGTTAAGCA | 540 | | |
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| QY | 541 | ACGGAAGAACTAAGGGTTAAACCAAGATGGCTTCTATTACCTGATCGCCACATTTGCTTC | 600 | | |
| Db | 541 | ACGGAAGAACTAAGGGTTAAACCAAGATGGCTTCTATTACCTGATCGCCACATTTGCTTC | 600 | | |
| QY | 601 | GGCATCATGAACATCGGGAGCGTACTCAAGACTATCTTCAAGCTATGCTGATGTG | 660 | | |
| Db | 601 | GGCATCATGAACATCGGGAGCGTACTCAAGACTATCTTCAAGCTATGCTGATGTG | 660 | | |
| QY | 661 | TTTAAACACAGATCAAAATCCCAAGTCTATTAACCTGATGAAGAGGAGGACAGGAAA | 720 | | |
| Db | 661 | TTTAAACACAGATCAAAATCCCAAGTCTATTAACCTGATGAAGAGGAGGACAGGAAA | 720 | | |
| QY | 721 | ACTGATCGGGCAATTTGATTCACATTTATTCATTAATGTGGGGGATTTTTCAGC | 780 | | |
| Db | 721 | ACTGATCGGGCAATTTGATTCACATTTATTCATTAATGTGGGGGATTTTTCAGC | 780 | | |
| QY | 781 | TCCGAGCTGTGAAGAAATTAAGCATTCAGGTGTCCAAACCTTCCCTCTGGATCCGATC | 840 | | |
| Db | 781 | TCCGAGCTGTGAAGAAATTAAGCATTCAGGTGTCCAAACCTTCCCTCTGGATCCGATC | 840 | | |
| QY | 841 | AAGATCGACATCTTTGGGGCTTTCAAAGTTAGGACATAGACTGAGACTCATTTGCTG | 900 | | |

| | | | |
|---|------|---|------|
| Db | 841 | AAAGTGGAGCTACTTTGGGGCTTCAAAAGCTTCAGSACATAGACTGAGACTCATTTTGGTG | 900 |
| QY | 901 | GAACATTAGCATGGATGCTCCTAGATGTTTGGAACTTCTTTAAAAATGATGATGCTAT | 960 |
| Db | 901 | GAACTATTAGCATGATGCTCCTAGATGTTTGGAACTTCTTTAAAAATGATGATGCTAT | 960 |
| QY | 961 | ACATGTGTAAAGCTACTAGTAGAGACATGGCCCGCAGGGTATGAAATCTCACACCCCTCTCTC | 1020 |
| Db | 961 | ACATGTGTAAAGCTACTAGTAGAGACATGGCCCGCAGGGTATGAAATCTCACACCCCTCTCTC | 1020 |
| QY | 1021 | TTTGAGCTGTACAGGTTGTGTATATGTAAAGCCCATAGTGTGATTTAATTCATGATGAT | 1080 |
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| QY | 1081 | TACACAACGGTTTTCACATTTTGTAAATGATTTTCTAGAAATTGAACAGATTGGAGAGCT | 1140 |
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| QY | 1141 | ATTCGGATGCTTATGAAAAAATTACACGCTGAGCTATGAGAGGGGGTCTACACTCTCTGGGT | 1200 |
| Db | 1141 | ATTCGGATGCTTATGAAAAAATTACACGCTGAGCTATGAGAGGGGGTCTACACTCTCTGGGT | 1200 |
| QY | 1201 | CTAACCCCTGGACACTGTGCCACTGAGACCTGTAATTAAGAGATGCGCATGTCTATTCGA | 1260 |
| Db | 1201 | CTAACCCCTGGACACTGTGCCACTGAGACCTGTAATTAAGAGATGCGCATGTCTATTCGA | 1260 |
| QY | 1261 | AAGAATATGATAGTGTGAAGGGTTAAGTTCCTTTTGAATGTACATTTGCGCTGGACCTGC | 1320 |
| Db | 1261 | AAGAATATGATAGTGTGAAGGGTTAAGTTCCTTTTGAATGTACATTTGCGCTGGACCTGC | 1320 |
| QY | 1321 | AAATATAGTCTTTTCTTCTCTAATGACGAGAGAAAAATATATGATTTTATATAAAGTCTA | 1380 |
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| QY | 1441 | AGTATTTGATTCAAAATATTTTAAAAATGTCACGTGTGACATATTTAAATGTTTTAAATG | 1500 |
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| RESULT 2 US-08-995-659-10 ; Sequence 10, Application US/08995659 ; Patent No. 6242213 ; GENERAL INFORMATION: ; APPLICANT: Anderson, Dirk M. ; APPLICANT: Galibert, Laurent ; APPLICANT: Maraskovsky, Eugene ; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB ; NUMBER OF SEQUENCES: 19 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Immunex Corporation, Law Department ; STREET: 51 University Street ; CITY: Seattle ; STATE: WA ; COUNTRY: USA ; ZIP: 98101 | | | |

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY:
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
US-08-995-659-10

Query Match 100.0%; Score 1630; DB 4; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CCGGCGTCCACAGAGAGGTCGCGTGCACCCGCGCTTCTGCACGCGGTCCGGCGCGC 60
61 CACCGCGCGCTCCGCTCCATGTTCTGCGCTCTGCGGCTGGAGTGGGCCAGGTGG 120
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121 TCTGCAGCATGCGTCTGTTCTCTGACTTTGAGAGGAGATGATCTCAACAGATATACAG 180
121 TCTGCAGCATGCGTCTGTTCTCTGACTTTGAGAGGAGATGATCTCAACAGATATACAG 180
121 TCTGCAGCATGCGTCTGTTCTCTGACTTTGAGAGGAGATGATCTCAACAGATATACAG 180
181 AAGACAGCACTACTGCTTTTATAGAACTGAGACTGCATGAAAGAGAGATTGGAGG 240
181 AAGACAGCACTACTGCTTTTATAGAACTGAGACTGCATGAAAGAGAGATTGGAGG 240
181 AAGACAGCACTACTGCTTTTATAGAACTGAGACTGCATGAAAGAGAGATTGGAGG 240
241 ACTGACTCTGGAGAGTGAAGACACACTACCTGACTCTCGAGGAGGATGAACAAACCT 300
241 ACTGACTCTGGAGAGTGAAGACACACTACCTGACTCTCGAGGAGGATGAACAAACCT 300
301 TTCAGGGGGCGGTGCAGAGAACTGCAACACTTGTGGGGCCACACGGCTTCTCAGAG 360

|||||
Db 301 TTCAGGGGGCGGTGCAGAGAACTGCAACACTTGTGGGGCCACACGGCTTCTCAGAG 360
|||
Qy 361 CTCGAGCTATGATGGAAGGCTCATGTTGATGTGGCCAGAGGAGAGCCTGAGGCC 420
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Db 361 CTCGAGCTATGATGGAAGGCTCATGTTGATGTGGCCAGAGGAGAGCCTGAGGCC 420
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Qy 421 AGCATTGGACACCTCAGCATCAATGCTGCGACATCCCATGGGGTTCCTTAAGTCA 480
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Db 421 AGCATTGGACACCTCAGCATCAATGCTGCGACATCCCATGGGGTTCCTTAAGTCA 480
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Qy 481 CTCTGCTCTTGGTACACAGATGAGGCTGGGCCAAGATCTTAACATGACGTTAAGCA 540
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Db 481 CTCTGCTCTTGGTACACAGATGAGGCTGGGCCAAGATCTTAACATGACGTTAAGCA 540
|||
Qy 541 ACGGAAACTAAGGTTAACCAGATGGCTTCTATTACCTGTACGCCACATTTGCTTC 600
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Db 541 ACGGAAACTAAGGTTAACCAGATGGCTTCTATTACCTGTACGCCACATTTGCTTC 600
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Qy 601 GGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTATGTCG 660
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Db 601 GGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTATGTCG 660
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Qy 661 TTAACACAGCATCAAAATCCCAAGTCTCATTAACCTGATGAAAGAGGAGCAGAAAA 720
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Db 661 TTAACACAGCATCAAAATCCCAAGTCTCATTAACCTGATGAAAGAGGAGCAGAAAA 720
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Qy 721 ACTGCTGGGCAATCTGCAATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGC 780
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Db 781 TCCGAGCTGTGAAGAAATTAGCTTACGATGTCACACCCCTCCCTGATGCCGATC 840
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Db 841 AAGATGCGAGCTACTTTGGGGCTTCAAGTTCAAGATCAGACATAGACTGATTTGCTG 900
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Db 901 GAACATTAGCATGATGCTGCTAGATGTTTGGAACTCTTAAAAAATGATGATGCTAT 960
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Qy 961 ACATGCTAAGACTACTTAAGACATGCGCCAGCGTATGAACACTACAGCCCTCTCTC 1020
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Db 961 ACATGCTAAGACTACTTAAGACATGCGCCAGCGTATGAACACTACAGCCCTCTCTC 1020
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Qy 1021 TTGAGCTGTACAGGTGTGTATATGTAAGTCCATAGTGTATGATTTGATGAT 1080
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Db 1021 TTGAGCTGTACAGGTGTGTATATGTAAGTCCATAGTGTATGATTTGATGAT 1080
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Db 1081 TACACAAGGTTTACAAATTTGTAATGATTTCCCTAGAAATTTGAACCAAGATTTGGAGAG 1140
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Qy 1141 ATTCCGATGCTTATGAAAACTTACAGTGAAGTATGGAAGGGGGTCCACAGTCTGGGT 1200
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Db 1261 AAGAAATGATAGTGAAGGTTAAGTCTTTGGAATGTTTACATGCGCTGGAGACTGCG 1320
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Db 1381 AAGTATATTTCAAGGTGTAATGTTTCTGTGCAAGTTTGTAAATTAATTTGTGCTAT 1440
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Db 1381 AAGTATATTTTCAGGCGTAAATGTTTTCGTGCGAAGGTTTGTAAATATATATGTCGTAT 1444
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Oy 1501 TACAGATGTTTAACTGGGCGACCTTGTAAATTCCTCGAAGGTAAGTCTGAGCTAAGGG 1560
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Oy 1561 GCAGAAATACGTTCTTCGTGACACACATGATGTTTATTTCTTATCTTTTAACTAATA 1620
Db 1621 GAGCTCTCAG 1630
Oy 1621 GAGCTCTCAG 1630
Db 1621 GAGCTCTCAG 1630

RESULT 3
US-09-215-649A-10
Sequence 10, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: RANKL

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: FEATURE:
: NAME/KEY: CDS
: LOCATION: 3..884
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-215-649A-10

Query Match      100.0%; Score 1630; DB 4; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGCTCCACACAGAGGGTCCGCTGCAACCCCGCGCCTTTCTGACACCGGCTCCGGGCGCCG 60
Db 1 CGGGCTCCACACAGAGGGTCCGCTGCAACCCCGCGCCTTTCTGACACCGGCTCCGGGCGCCG 60
QY 61 CACCGCGCGCCTCCCGGCTCCACATGTTCCCTGGGCCCTCTGAGGCTGGGAGCTGGGCGCAGTGG 120
Db 61 CACCGCGCGCCTCCCGGCTCCACATGTTCCCTGGGCCCTCTGAGGCTGGGAGCTGGGCGCAGTGG 120
QY 121 TCTGCAGCAGCTGCCTCTGTTCTGTTCTGATCTTTCGAGCGCAGATGAGATCTTAACAGAAATATCAG 180
Db 121 TCTGCAGCAGCTGCCTCTGTTCTGTTCTGATCTTTCGAGCGCAGATGAGATCTTAACAGAAATATCAG 180
QY 181 AAGAGAGACATCACAGCTTTTATAGAAATCCTGAGAGCTCCATGAAACGAGATTTTGCAGG 240
Db 181 AAGAGAGACATCACAGCTTTTATAGAAATCCTGAGAGCTCCATGAAACGAGATTTTGCAGG 240
QY 241 ACTGCAGCTCTGGAGAGTGAAGACACACACTACCTGACTCCTGACGAGGAGATGAACAAGCCT 300
Db 241 ACTGCAGCTCTGGAGAGTGAAGACACACTACCTGACTCCTGACGAGGAGATGAACAAGCCT 300
QY 301 TTTCAGGGGGCGCTGCAGAAAGAACTGCAAACATTTGGGGGCGCACAGGCGCTTCTCAGAGG 360
Db 301 TTTCAGGGGGCGCTGCAGAAAGAACTGCAAACATTTGGGGGCGCACAGGCGCTTCTCAGAGG 360
QY 361 CTCGAGCTATGATGGAAGGGCTCATGTTGGATGTGGCCAGCGAGGCAAGCCTGAGGCC 420
Db 361 CTCGAGCTATGATGGAAGGGCTCATGTTGGATGTGGCCAGCGAGGCAAGCCTGAGGCC 420
QY 421 AGCCATTGTCACACTCCACATCATGCTGTGCCAGCATCCCATCGGGTTCCCTAAAGTGA 480
Db 421 AGCCATTGTCACACTCCACATCATGCTGTGCCAGCATCCCATCGGGTTCCCTAAAGTGA 480
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Db 481 CTCCTGCTGTTGGTATGACAGATGCAAGGCTGGGGCAAGATCTCTAAACATGAGAGTTAAGCA 540
QY 541 ACGGAAAACCTAAGGTTTAAACAAGATGCTTATTAACCTGTGACGCCAACATTTGCTTTC 600
Db 541 ACGGAAAACCTAAGGTTTAAACAAGATGCTTATTAACCTGTGACGCCAACATTTGCTTTC 600
QY 601 GGCATCATGAACATTCGGGAAGCGTATCCATGACAGACTATTTGAGCTGATGGTATGTGG 660
Db 601 GGCATCATGAACATTCGGGAAGCGTATCCATGACAGACTATTTGAGCTGATGGTATGTGG 660
QY 661 TTAAACACGACATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGACGACGAAAA 720
Db 661 TTAAACACGACATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGAGGACGACGAAAA 720
QY 721 ACTGGTGGGGCAATTCGAAATTCACATTTTATTCATTAATGTTGGGGATTTTGAAG 780
Db 721 ACTGGTGGGGCAATTCGAAATTCACATTTTATTCATTAATGTTGGGGATTTTGAAG 780
QY 781 TCCGAGCTGTGAAGAAATTTAGCATTCAGAGTGTCCAAACCTTCCTGCTGATCCGAGT 840
Db 781 TCCGAGCTGTGAAGAAATTTAGCATTCAGAGTGTCCAAACCTTCCTGCTGATCCGAGT 840
QY 841 AAGATGCAAGTACTTTGGGGCTTTCAAGTTGAGACATAGACTAGACTCATTTTCGTG 900
Db 841 AAGATGCAAGTACTTTGGGGCTTTCAAGTTGAGACATAGACTAGACTCATTTTCGTG 900
QY 901 GAACATTTACATGAAGTGTCTGATGTTTGAAGAACTTTAAAAAATGATGATGTAT 960
Db 901 GAACATTTACATGAAGTGTCTGATGTTTGAAGAACTTTAAAAAATGATGATGTAT 960

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Db 901 GAACATTAGCATGATGCTAGATGTTGGAACTTCTTAAAAAATGATGATGCTAT 960
Qy 961 ACATGTGTAAAGACTACTAAGAGACATGGCCACGGTGTATGAACCTACAGCCCTCTC 1020
Db 961 ACATGTGTAAAGACTACTAAGAGACATGGCCACGGTGTATGAACCTACAGCCCTCTC 1020
Qy 1021 TTGAGCCTGTACAGGTTGTATATGTAAAGTCCATAGGTGATGATTAAGATTGATGAT 1080
Db 1021 TTGAGCCTGTACAGGTTGTATATGTAAAGTCCATAGGTGATGATTAAGATTGATGAT 1080
Qy 1081 TACACACGCGTTTACAAATTTTGAATGATTTCTGAAATGAACCAAGATTGGGAGAGT 1140
Db 1081 TACACACGCGTTTACAAATTTTGAATGATTTCTGAAATGAACCAAGATTGGGAGAGT 1140
Qy 1141 ATTCCGATGCTTATGAAAAAATTACACGTGAGCTATGGAAGGGGGTCCACGCTCTGGGT 1200
Db 1141 ATTCCGATGCTTATGAAAAAATTACACGTGAGCTATGGAAGGGGGTCCACGCTCTGGGT 1200
Qy 1201 CTAAACCCCTGCACATGTGCGACCTGAGAACCTTGAATTAAGAGATGCCATGCTATGCA 1260
Db 1201 CTAAACCCCTGCACATGTGCGACCTGAGAACCTTGAATTAAGAGATGCCATGCTATGCA 1260
Qy 1261 AAGAAATGATAGTGTGAAGGGTTAAGTTCTTTGAATTTGTAATGCGCTGGAGACTGC 1320
Db 1261 AAGAAATGATAGTGTGAAGGGTTAAGTTCTTTGAATTTGTAATGCGCTGGAGACTGC 1320
Qy 1321 AAATTAAGTCTTTTCTTATGAGAGAGAAAAATATATGATTTTATATATATGCTTA 1380
Db 1321 AAATTAAGTCTTTTCTTATGAGAGAGAAAAATATATGATTTTATATATATGCTTA 1380
Qy 1381 AAGTTAATTTGAGGTGATATGTTTCTGTGCAAAAGTTTGTAAATTAATTTGCTAT 1440
Db 1381 AAGTTAATTTGAGGTGATATGTTTCTGTGCAAAAGTTTGTAAATTAATTTGCTAT 1440
Qy 1441 AGTATTTGATTTAAATTTTAAATGCTGCACTGATGACATATTTATTTTAAAG 1500
Db 1441 AGTATTTGATTTAAATTTTAAATGCTGCACTGATGACATATTTATTTTAAAG 1500
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Db 1501 TACAGATGATTTAACTGTGCTGCACTTTGTAATTTCCCTGAAGTACTGCTAAGGG 1560
Qy 1561 GCAGATGATGTTTGTGAGCACATGATGATTTTCTTTATTTTAACTTAATA 1620
Db 1561 GCAGATGATGTTTGTGAGCACATGATGATTTTCTTTATTTTAACTTAATA 1620
Qy 1621 GAGTCTTCAG 1630
Db 1621 GAGTCTTCAG 1630

RESULT 4
US-08-842-842-6
Sequence 6, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842

FILED DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 158..1105
US-08-842-842-6
Query Match 99.9% Score 1628.4; DB 2: Length 2295;
Best Local Similarly 99.9% Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCGGGCTCCACACAGAGGGTCCGCTGCACACCCGCGCTTCTGCAACCGGCTCCGGCGCGC 60
Db 222 CCGGGCTCCACACAGAGGGTCCGCTGCACACCCGCGCTTCTGCAACCGGCTCCGGCGCGC 281
Qy 61 CACCGCGCGCTCCCGCTGCATGTTCTGSCCTCTGCGGGCTGGAGCTGGGCCAGGTGG 120
Db 282 CACCGCGCGCTCCCGCTGCATGTTCTGSCCTCTGCGGGCTGGAGCTGGGCCAGGTGG 341
Qy 121 TCTGAGCATGCTCTGTTCTGTTACTTTGAGGGCGAGTGGATCTTACAGAAATATACAG 180
Db 342 TCTGAGCATGCTCTGTTCTGTTACTTTGAGGGCGAGTGGATCTTACAGAAATATACAG 401
Qy 181 AAGACAGCATCTACTGCTTTTATAGAAATCTGAGACTCCATGAAAGACAGATTGGCAGG 240
Db 402 AAGACAGCATCTACTGCTTTTATAGAAATCTGAGACTCCATGAAAGACAGATTGGCAGG 461
Qy 241 ACTGAGCTCTGAGAGATGAGACACACTACTGACTCTCTGAGAGAGATGAACAAAGCCT 300
Db 462 ACTGAGCTCTGAGAGATGAGACACACTACTGACTCTCTGAGAGAGATGAACAAAGCCT 521
Qy 301 TTGAGGGGGCGGTGACAGAAAGGAACTGCACACATTTGTGGGGCCACAGCGCTTCTCAGGAG 360
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Qy 361 CTCAGCTATGATGGAAGGCTCATGTTGATGTGGTGGCCACAGGAGCAAGCCCTGAGGCC 420
Db 582 CTCAGCTATGATGGAAGGCTCATGTTGATGTGGTGGCCACAGGAGCAAGCCCTGAGGCC 641
Qy 421 AGCCATTTGCACACCTCACCATCAATGCTGCGACGATCCCATGGGGTTCCTATAAAGTCA 480
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Qy 601 GGCATCATGAACATGGGGAAGGCTACCTATGCTGCTGAGTGGATGATGATGATG 660
Db 822 GGCATCATGAACATGGGGAAGGCTACCTATGCTGCTGAGTGGATGATGATGATGATG 881
Qy 661 TTAAACACGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGACACAGAAA 720
Db 882 TTAAACACGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGAGACAGAAA 941
Qy 721 ACTGTCGCGGCAATTCGATTCACATTTTATTCATTAATGTTGGGGATTTTTCACAG 780
Db 942 ACTGTCGCGGCAATTCGATTCACATTTTATTCATTAATGTTGGGGATTTTTCACAG 1001

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| OY | 781 | TCCGACGTGGTGAAGAAATTTACCATTCGAGGTGTCACACCCCTCCCTGCTGGATCCGAGAC | 840 |
| Db | 1002 | TCCGACCTGGTGAAGAAATTTACCATTCAGGTGTCCACACCCCTCCCTGCTGGATCCGAGAC | 1061 |
| OY | 841 | AAGATGCGAGGTCTTTGGGGCTTTCAAAGTTCAAGSACATAGACTGACTTATTCGTG | 900 |
| Db | 1062 | AAGATGCGAGGTCTTTGGGGCTTTCAAAGTTCAAGSACATAGACTGACTTATTCGTG | 1121 |
| OY | 901 | GAACATTAGCAGTGGATGTCCTTAGATGTTTGGAACTTTTAAAAAATGATGATGTCCTAT | 960 |
| Db | 1122 | GAACATTAGCAGTGGATGTCCTTAGATGTTTGGAACTTTTAAAAAATGATGATGTCCTAT | 1181 |
| OY | 961 | ACATGTGTAGACTACTATAAGACAGCATGGGCCCGGCTGTATGATAAACTCACAGCCCTCTCTC | 1020 |
| Db | 1182 | ACATGTGTAGACTACTATAAGACAGCATGGGCCCGGCTGTATGATAAACTCACAGCCCTCTCTC | 1241 |
| OY | 1021 | TTGAGCCTGTACAGGTGTGTATATGTAAAGTCCATAGGTATGTTAGATTCAATGATGAT | 1080 |
| Db | 1242 | TTGAGCCTGTACAGGTGTGTATATGTAAAGTCCATAGGTATGTTAGATTCAATGATGAT | 1301 |
| OY | 1081 | TACCAACGGTTTTACAAATTTTGTATATGATTTTCCAGAAATTAAGACACGATTTGGAGAGGT | 1140 |
| Db | 1302 | TACCAACGGTTTTACAAATTTTGTATATGATTTTCCAGAAATTAAGACACGATTTGGAGAGGT | 1361 |
| OY | 1141 | ATTCCGATGCTTATGAAAACTTACACGTGAGCTATGGAAGGGGGTCCACAGTCTCTGGGT | 1200 |
| Db | 1362 | ATTCCGATGCTTATGAAAACTTACACGTGAGCTATGGAAGGGGGTCCACAGTCTCTGGGT | 1421 |
| OY | 1201 | CTAACCCCTGGACATGTGGCCACTGAGAACCTTGAATTAAGAGATGGCATGTCATTTGCA | 1260 |
| Db | 1422 | CTAACCCCTGGACATGTGGCCACTGAGAACCTTGAATTAAGAGATGGCATGTCATTTGCA | 1481 |
| OY | 1261 | AAGAAATGATGTGTGAAGGGTTAAGTCTTTTGAATGTGTACATTGGCGTGGGACCTGTC | 1320 |
| Db | 1482 | AAGAAATGATGTGTGAAGGGTTAAGTCTTTTGAATGTGTACATTGGCGTGGGACCTGTC | 1541 |
| OY | 1321 | AAATTAAGTCTTTTTTCTAATGAGAGAGAAAAATATATGATTTTATATATATGCTTA | 1380 |
| Db | 1542 | AAATTAAGTCTTTTTTCTAATGAGAGAGAAAAATATATGATTTTATATATATGCTTA | 1601 |
| OY | 1381 | AAGTTATATTTTCAGCTGTAATGTTTCTGTGCAAACTTTTGTAAATTAATTAATTTGCTAT | 1440 |
| Db | 1602 | AAGTTATATTTTCAGCTGTAATGTTTCTGTGCAAACTTTTGTAAATTAATTAATTTGCTAT | 1661 |
| OY | 1441 | AGTATTTATTCCAAAATATTAAAAATGTCTCACTGTGACATATTAAATGTTTTAAATG | 1500 |
| Db | 1662 | AGTATTTATTCCAAAATATTAAAAATGTCTCACTGTGACATATTAAATGTTTTAAATG | 1721 |
| OY | 1501 | TACAGATGATTTTAACTGTCGTCACCTTTGTATATTCCTCCGTGAAGGTACTGCTACTAAGGGG | 1560 |
| Db | 1722 | TACAGATGATTTTAACTGTCGTCACCTTTGTATATTCCTCCGTGAAGGTACTGCTACTAAGGGG | 1781 |
| OY | 1561 | GGAGAAATCTGTTCTGCTGGTGACCAAGATGTATTTATTTCTTTATCTTTTAACTTAATA | 1620 |
| Db | 1782 | GGAGAAATCTGTTCTGCTGGTGACCAAGATGTATTTATTTCTTTATCTTTTAACTTAATA | 1841 |
| OY | 1621 | GAGTCTTCAG 1630 | |
| Db | 1842 | GAGTCTTCAG 1851 | |
| RESULT 5 | | | |
| US-09-052-521C-1 | | | |
| ; Sequence 1, Application US/09052521C | | | |
| ; Patent No. 6316408 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Boyle, William J. | | | |
| ; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors | | | |
| ; FILE REFERENCE: A-451Btv | | | |
| ; CURRENT APPLICATION NUMBER: US/09/052, 521C | | | |
| ; CURRENT FILING DATE: 1998-03-30 | | | |
| ; PRIOR APPLICATION NUMBER: 08/860, 855 | | | |

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1  PRIOR FILING DATE: 1997-06-23
2  PRIOR APPLICATION NUMBER: 08/842,842
3  PRIOR FILING DATE: 1997-04-16
4  NUMBER OF SEQ ID NOS: 40
5  SOFTWARE: PatentIn Ver. 2.1
6  SEQ ID NO 1
7  LENGTH: 2295
8  TYPE: DNA
9  ORGANISM: Mouse
10 FEATURE:
11 NAME/KEY: CDS
12 LOCATION: (158)..(1105)
13 OS-09-052-521C-1

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[illegible]

Db 1002 tccgagcgtgctgaagaatcagcaltcagtgctccaaacctccctgctgagtcgcgagtc 1061
Qy 841 AAGATCGACGACTACTTGGGCTTTCAAGATTCAGACATAGACATGACATTTGCTG 900
Db 1062 aagatgagcagctactcttggtgcttcaaaagctcagagacatagcagacccatctcg 1121
Qy 901 GAACATTAGCATGATGCTCAGATGTTTGGAAACTTCTTAAAAATGATGATGCTAT 960
Db 1122 gaacattagcagctgagctcagagctgctggaactcttcaaaaatgagatgctcat 1181
Qy 961 ACATGTGTAACTACTAAGACATGCGCCACGCTGTATGAACCTCACAGCCCTCTCTC 1020
Db 1182 acatgtgtaaactactaagagacatg9ccacggtgatgaaactcacagccctctctc 1241
Qy 1021 TTGAGCCCTGTACAGTGTGTATGTAAAGTATGATGATGATGATGATGATGAT 1080
Db 1242 ctgagccctgctcaggtctgctgatactgaagccacatagtgatgatacagtgat 1301
Qy 1081 TACACACAGGTTTACATTTTGAATGATTTCTAGATTTGAACACAGATTGGAGAGGT 1140
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Qy 1141 ATTCCGATGCTTATGAAAAATTACAGGTGAGCTATGAGAGGGGCTCACAGTCTGCGT 1200
Db 1362 attccgattgcttaagaaaactacacgtgagctatgaa9gg9gtcacagctcctggt 1421
Qy 1201 CTAACCCCTGGACATGTCGCACTGAGAACCTTGAATTAAGAGATGGCATGCTATTGCA 1260
Db 1422 ctaaaccttgagacatgctgacacgtgagaaacctgaatgaag9gagtgcaagtcacatgca 1481
Qy 1261 AAGAAATCATAGTGTGAAGGCTTAACTTTTGAATTTTACATTGGCGTGGAGACCTGC 1320
Db 1482 aagaaatcatagtgctgaag9gttaagttcttctgtaattgtaactgctgctggagacctgc 1541
Qy 1321 AAATAAGTCTTTTCTTATATGAGAGAGAAAAATATATATTTTATATATGCTA 1380
Db 1542 aataaagctcttcttctcctaaagag9gaaataatatactatcttataatagctta 1601
Qy 1381 AAGTATATTTACAGTGAATGTTTCTGTGCAAGTTTGTAAATTAATATTTGCTAT 1440
Db 1602 aagtaatactcaggtgctaaagcttctctgcaaaagttctgtaaatctatcttctgctat 1661
Qy 1441 AGTATTTGATTTCAAAATATTTAAATGTCTCACTGTTGACATATTTAATGTTTAAATG 1500
Db 1662 agtattctgattcaaaaataatlaaaatgctcactgctgacataatlaatgctttaaag 1721
Qy 1501 TACAGATGATTTAACTGCTGCACTTTGTATTTCCCTGAAGGTAAGTCTAAGCTAAGGG 1560
Db 1722 tacagatgatttaacggtgacactctgtaattccctgaaagtaacctgtaagcctaa999 1781
Qy 1561 GCAGAACTACTGTTTCTGTGACACATAGTATGTTTATTTCTTTTAACTTATA 1620
Db 1782 gcagaaactactgcttctggtgacacatagttatcttcttatacttctttaaactaata 1841
Qy 1621 GAGTCTTACG 1630
Db 1842 gagctctcag 1851

RESULT 6
US-08-989-362-1
Sequence 1, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens: Related
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 125..1072
US-08-989-362-1

Query Match 99.1%; Score 1615.8; DB 4; Length 2191;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CCGGCGCTCCACACAGAGGTCGCTGACACCCGCGCTTTCGACCGCGCTCCGCGCGC 60
Db 189 CCGGCGCTCCACACAGAGGTCGCTGACACCCGCGCTTTCGACCGCGCTCCGCGCGC 248
Qy 61 CACCGCGCGCTCCGCTCCATGTTCTGCGCGCTCTGGGGGCTGGAGCTGGCGCAGGTG 120
Db 249 CACCGCGCGCTCCGCTCCATGTTCTGCGCGCTCTGGGGGCTGGAGCTGGCGCAGGTG 308
Qy 121 TCTGACGATCGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 180
Db 309 TCTGACGATCGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 368
Qy 181 AAGACGACACTGCTGTTTATGAACTCTGAGACTTCATGAAACGCAAGATTTGACAG 240
Db 369 AAGACGACACTGCTGTTTATGAACTCTGAGACTTCATGAAACGCAAGATTTGACAG 428
Qy 241 ACTGACTGTGAGAGTGAAGACACACTGACTGACTGCTGCTGAGAGATGAACAGGCT 300
Db 429 ACTGACTGTGAGAGTGAAGACACACTGACTGACTGCTGCTGAGAGATGAACAGGCT 488
Qy 301 TTCAGGGGCGGTGACAGAGAACTGCACACATTTGGGGCCACAGCGCTTCTCAGAG 360
Db 489 TTCAGGGGCGGTGACAGAGAACTGCACACATTTGGGGCCACAGCGCTTCTCAGAG 548
Qy 361 CTCAGCTATGATGAGAGGCTGATGTTGATGTTGAGGCTGAGGCTGAGGCTGAGGCT 420
Db 549 CTCAGCTATGATGAGAGGCTGATGTTGATGTTGAGGCTGAGGCTGAGGCTGAGGCT 608
Qy 421 AGCCATTGACACCTCACCATCAATGCTGCCAGCATCCATGGGTTCCCATTAAGTCA 480
Db 609 AGCCATTGACACCTCACCATCAATGCTGCCAGCATCCATGGGTTCCCATTAAGTCA 668
Qy 481 CTCTGCTCTTGGTACACGATGAGAGGCTGGGCCAAGATCTTAACATGACGTTAAGCA 540

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Db 669 CTCTGCTCTTGGTACACGATCGAGGCTGGCCAAAGATCTCTAACATGACGTTAAGCA 728
OY 541 ACGGAAACCTAAGGGTTAACCAGATGGCTTCTATTCCTGCTACGGCAACATTTGCTTC 600
Db 729 ACGGAAACCTAAGGGTTAACCAGATGGCTTCTATTCCTGCTACGGCAACATTTGCTTC 788
OY 601 GGCATCATGAACATCGGGAAGGCTACCTACAGATATCTTCAGCTGATGGTATGTCG 660
Db 789 GGCATCATGAACATCGGGAAGGCTACCTACAGATATCTTCAGCTGATGGTATGTCG 848
OY 661 TTTAAACCCAGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGACACGAAAA 720
Db 849 TTTAAACCCAGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGACGAAAA 908
OY 721 ACTGCTGGGCAATTCGAAATTCACCTTTATTCATTAATGTTGGGGATTTTTCAGC 780
Db 909 ACTGCTGGGCAATTCGAAATTCACCTTTATTCATTAATGTTGGGGATTTTTCAGC 968
OY 781 TCCGAGCTGTAAGAAATTTAGCATTCAGTGTCCAAACCCCTCCCTGCTGATCCGATC 840
Db 969 TCCGAGCTGTAAGAAATTTAGCATTCAGTGTCCAAACCCCTCCCTGCTGATCCGATC 1028
OY 841 AAGATGCGAGCTACTTTGGGCTTCAAACTTCAGGACATGAGACTGACATTTGCTG 900
Db 1029 AAGATGCGAGCTACTTTGGGCTTCAAAAGTTTCAGGACATGAGACTGACATTTGCTG 1088
OY 901 GAACATTAAGCATGATGATGCTAGATGTTTGAACCTTCTTAAAAATGATGATGCTAT 960
Db 1089 GAACATTAAGCATGATGATGCTAGATGTTTGAACCTTCTTAAAAATGATGATGCTAT 1148
OY 961 ACATGCTGAAGACTACTTAAGAGACATGGCCACGGGTATGAACCTCACAGCCCTCTCTC 1020
Db 1149 ACATGCTGAAGACTACTTAAGAGACATGGCCACGGGTATGAACCTCACAGCCCTCTCTC 1208
OY 1021 TTGAGCCTGTACAGTGTGTATATGTAAGTCCATAGCTATGTATGATTCATGCTAT 1080
Db 1209 TTGAGCCTGTACAGTGTGTATATGTAAGTCCATAGCTATGTATGATTCATGCTAT 1268
OY 1081 TACACAAAGGTTTACATTTTGTATATGATTTCC - AGAATTGAACCGATTGGGAGAG 1139
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OY 1200 TCTAACCCCTGGACATGTCGCCACTGAGAACCTTGAATTAAGAGATGCATGTCATGC 1259
Db 1389 TCTAACCCCTGGACATGTCGCCACTGAGAACCTTGAATTAAGAGATGCATGTCATGC 1448
OY 1260 AAGAAATGATAGTGAAGGGTTAAGTCTTTTGAATTTGATTCAGTCCGCTGGAGCTG 1319
Db 1449 AAGAAATGATAGTGAAGGGTTAAGTCTTTTGAATTTGATTCAGTCCGCTGGAGCTG 1508
OY 1330 CAATTAAGTCTTTTCTTAATGAGAGAGAAAAATATGATTTTATTAATGCT 1379
Db 1509 CAATTAAGTCTTTTCTTAATGAGAGAGAAAAATATGATTTTATTAATGCT 1568
OY 1380 AAGATTAATTCAGTGTAATGTTTCTGTCGCAAAAGTTTGAATTAATTAATGCTGA 1439
Db 1569 AAGATTAATTCAGTGTAATGTTTCTGTCGCAAAAGTTTGAATTAATTAATGCTGA 1628
OY 1440 TGAATTTGATTCAAAAATTTAAAAATGTCACGTGTAATTAATTAATGCTTTAAAT 1499
Db 1629 TGAATTTGATTCAAAAATTTAAAAATGTCACGTGTAATTAATTAATGCTTTAAAT 1688
OY 1500 GTACAGATGATTAACCTGGTCACTTTGTAAATCCCTGAAGGTAAGTGTACGTAAGG 1559
Db 1689 GTACAGATGATTAACCTGGTCACTTTGTAAATCCCTGAAGGTAAGTGTACGTAAGG 1748
OY 1560 GGCAGAAATCTGTTCTGCTGACACATGATGATTAATTTCTTAATCTTTAACTTAAT 1619
Db 1749 GGCAGAAATCTGTTCTGCTGACACATGATGATTAATTTCTTAATCTTTAACTTAAT 1808
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OY 1620 AGAGTCTTCAG 1630
Db 1809 AGAGTCTTCAG 1819

RESULT
US-09-521C-3
; Sequence 3, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding proteins and Receptors
; FILE REFERENCE: A-451b-v
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2271
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (185)..(1135)
US-09-052-521C-3

Query Match 57.6%; Score 939.6; DB 4; Length 2271;
Best Local Similarity 78.1%; Pred. No. 4,5e-247;
Matches 1285; Conservative 0; Mismatches 314; Indels 47; Gaps 11;

OY 1 CCGGCGTCCACAGAGGGTCCGCTGACACCCCGGCGCTTCGACCGGGCTCCGGCGCGC 60
Db 249 ccgagccgcgcgagagagagagagagagagagagagagagagagagagagagagagag 305
OY 61 CACCGCGCGCTCCCGCTCCATGTTTCCGCGCCCTCTGCGGCTGGAGCTGGGCCAGGTGG 120
Db 306 ccccgccgcgcctcccgctccatggttccgagagagagagagagagagagagagagagag 365
OY 121 TCTGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 366 tctgagcgcgcgcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 425
OY 181 AAGACAGACATCAGCTTTATATGAAATCTGAGACCTCATGAAAAACGAGATTTGCAG 240
Db 426 aagatgacacacacacacacacacacacacacacacacacacacacacacacacacacac 485
OY 241 ACTGACTCTGAGAGAGTGAAGACAC-----ACTACTGACTCTGCGAGAGATGAAC 294
Db 466 acacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 545
OY 295 AAGCTTTCAGGGGCGCTGCAAGAAAGTGCACACATGTTGGGGGCGACAGGCGCTTCT 354
Db 466 aagccttcagggcgctgcaagaaagtgcacacatggtggggcgacagggcgcttctct 414
OY 355 CAGGAGCTCCAGCTATGATGGAAGGCTCATGTTGATGTTGAGTGGCCAGGAGGAGCCTG 414
Db 606 gagcagagagagagagagagagagagagagagagagagagagagagagagagagagag 665
OY 415 AGGCCAGGCAATTTGCACACCTCACCATCAATGCTGCGACATCCCATCGGTTCCCTA 474
Db 666 aagccagagccttctgcatcactatcactatcactatcactatcactatcactatcactat 725
OY 475 AAGTCACTGTGCTCTTGTGTCACAGATCGAGGCTGGGCGCAAGATCTCTAAGATGAGT 534
Db 726 aagtgagtgctgctcttctgtgacacacacacacacacacacacacacacacacacacac 785
OY 535 TAAGCAAGGAAATAAGGGGTTTAACCAAGATGCTTCTATTAATCTGTACGCAACATTT 594
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|---|-----|--|-----|
| OY | 61 | CACCGCCGCTCCGCATCATGTCTCCGGCCTCCCTGGGGGCTGGAGACTGCGGCAAGTGG | 120 |
| Dd | 122 | CCCCGCCGCTCCCGCTCATGTTCGTGGCCCTCTGGGGCTGGGGCTGGGCCAGTTG | 181 |
| OY | 121 | TCTGCAGCATCGCTCTGTCTCTGACTTTTGACGCGAGATGATTCCTAACAGAAATCAG | 180 |
| Dd | 182 | TCTGCAGGTGCGCCTTTCTTCTATTTCAGACGCGAGATGATTCCTAATGAAATTCAG | 241 |
| OY | 181 | AAGACAGCACTCACTGCTTTTAAGAATCTGAGACTCATGAATAACGAGATTTGCAG | 240 |
| Dd | 242 | AAGATGGCACTCACTGCATTTATGAAATTTGAGACTCCATGAAAAATGCAGATTTTCAAG | 301 |
| OY | 241 | ACTGCAGCTTGGAGAGTGAACAC-----ACTACTGACTCTCCGAGGAGATGAAC | 294 |
| Dd | 302 | ACACAACCTCTGGAGAGTCAAMATCAAAAATAAATTAATCTGATTAATGAGAGATTAAC | 361 |
| OY | 295 | AAGCTTTACAGGGGGCCGTGAGAGGACATGCACAACATTTGGGGCCACAGCGTTCT | 354 |
| Dd | 362 | AGGCTTTTACAGAGACTGTGTCAAAAGATTTACAACTATCTGTTGATTCACAGCAATCA | 421 |
| OY | 355 | CAGAGCTCCAGCTATGATGAGAGGCTCATGTTGGATGTGGCCACGAGCAAGCTTG | 414 |
| Dd | 422 | GAGCAGAAAGCGATGGTGTGATGGCTCATGTTAGATCTGGCCACAGAGGAGCAAGTTG | 481 |
| OY | 415 | AGGCCAGCACTTTGCACACTCACACATCAATGCTGCAGATCCCATGGGGTTCCATA | 474 |
| Dd | 482 | AAGCTCACACTTTCCTATCTACTATTAATGACCACGACATCCCATCTGGTTCCATA | 541 |
| OY | 475 | AAGTACCTCTGCTCTTGGTACACAGATCGAGGCTGGGCGAAGATCTCAACATGACGT | 534 |
| Dd | 542 | AAGTAGTCTGCTCTTGTGTRACATGATCGGGGTTGGGCCAAGATCTCCAACATGACTT | 601 |
| OY | 535 | TAAACAGCGAAMAATAAGGTTAAACCAAGATGCTTATTTACCTGACCCAACTTT | 594 |
| Dd | 602 | TTAGCAATGGAAAACTAATAGTTATTCAGATGAGCTTTATTTACCTGTATGCCAACTTT | 661 |
| OY | 595 | GCTTTCCGATATTAACATTCGGGAACCGTACACAGATATCTCAGCTGATGCTGT | 654 |
| Dd | 662 | GCTTTTCGATATTAACATTCGGGAACCGTACACAGATATCTCAGCTGATGCTGT | 721 |
| OY | 655 | AGTGTGTTAAACACAGATCAAAATCCCAAGTTCTCATATACCTGATGAAGAGGAGACA | 714 |
| Dd | 722 | AGTGTGTTAAACACAGATCAAAATCCCAAGTTCTCATATACCTGATGAAGAGGAGACA | 781 |
| OY | 715 | CGAANAACGTGCGGCAATTCGAATTCACATTTATTCATAAATGTTGGGGATTTT | 774 |
| Dd | 782 | CGAAGTATGTCAGAGGAATTCGAATTCACATTTATTCATAAATGTTGGGGATTTT | 841 |
| OY | 775 | TCAAGCTCGGAGCTGTGAAGAAATTAAGATCAGSTGCCAACCCCTCCGCTGATC | 834 |
| Dd | 842 | TTAAGTTAGGCTGTGAAGGAAATTAAGATCAGSTGCCAACCCCTCCGCTGATC | 901 |
| OY | 835 | CGGATCAAGTGCAGCTACTTTGGGGCTTTCAAAGTTTCAGACATATGACGA | 887 |
| Dd | 902 | CGGATCAAGTGCAGCTACTTTGGGGCTTTCAAAGTTTCAGACATATGACGA | 954 |
| RESULT 9 US-08-995-659-12 ; Sequence 12, Application US/0895659 ; Patent No. 6242213 ; GENERAL INFORMATION: ; APPLICANT: Anderson, Dirk M. ; APPLICANT: Gallibert, Laurent ; APPLICANT: Marasovsky, Eugene ; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappab ; NUMBER OF SEQUENCES: 19 ; CORRESPONDENCE ADDRESSES: ; ADDRESSEE: Immunex Corporation, Law Department ; STREET: 51 University Street ; CITY: Seattle ; STATE: WA ; COUNTRY: USA | | | |

```

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US5N 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US5N 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US5N 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-995-659-12

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| QY | 295 | AAGCCTTTACAGGGGCGCCGTCAGAAAGAAATGCAACACATTTGTGGGGCCACAGGGCTTCT | 35 |
| Db | 362 | AGGCCTTTCAAGAGAGCTGTGCAAAAGAAATTACACACATATCTTTGGATCACAGACATCA | 422 |
| QY | 335 | CAGAGCTTCAGACTATGATGGAAGGCTTCATGGTTGGATGTGGCCCGACGAGCAAGCCTG | 414 |
| QY | 415 | AGGCCACCGCAATTTGSCAACACTTCAACATCATTGTGCTGCCAGATCCCATCGGGTCCATA | 474 |
| Db | 422 | GAGCGAGAGAAAAGCGATGGTGGATGGCTCATGGTTAGATCTGCGCAAGAGAGCAAGCTTG | 481 |
| QY | 475 | AAGTCACTCTGCTCCTCTTGGTATACACGATCGAGGCTGGGCCAAGATCTCTAACATGACGT | 534 |
| Db | 542 | AAGTAGCTGTGCTGCTTGGTACCATGATTCGGGGTTGGGGCCAAATCTCCAAACATGACTT | 601 |
| QY | 535 | TAAAGCAAGGAAAATTAAGGGTTAAACCAAGATGGCTTCTATTACCTGTAGCCCAACTTT | 594 |
| Db | 602 | TTAGCAATAAGAAAATTAATTAATGATGCGATGGCTTTTATTACCTGTATGCGCCAACTTT | 661 |
| QY | 595 | GCTTTCCGCGATCATGAAACATCGGGAAGCGTACACCTATCATCTGAGTGTGATG | 654 |
| Db | 662 | GCTTTCCGATCATGAAACATCGGGAAGCGTACACCTATCATCTGAGTGTGATG | 721 |
| QY | 655 | ATGTGCTTTAAACACAGCATCAAAATCCCAAGTCTCATTAACCTGATGAAGAGAGAGCA | 714 |
| Db | 722 | AGCTCACTTAAACACAGCATCAAAATCCCAAGTCTCATTAACCTGATGAAGAGAGAGCA | 781 |
| QY | 715 | CGAAAACCTGGTGGGGCAATCTGAATTCACCTTTATTCATTAATGTTGGGGGATTTT | 774 |
| Db | 782 | CCAAAGTATTTGGTCAAGGCAATTTCTAAATTCATTTTATTCATTAACCTGTGGTGATTTT | 841 |
| QY | 775 | TCAGAGCTTCGAGCTGGTGAAAGAAATTAGCATTCAGGTGTCCCAACCTTCCCTGCTGATC | 834 |
| Db | 842 | TTAAGTTCAGGCTGTGGAGAGAAATCAGCATCGAGGTCTCCAAACCCCTCTTACTGGATC | 901 |
| QY | 835 | CGGATCAAGATCCGACGCTACTTTGGGGCTTTCAAGATTCAGAGCATGACTGA | 887 |
| Db | 902 | CGGATCAAGATCCGACGCTACTTTGGGGCTTTTAAAGTTGAGATATGATTGA | 954 |
| RESULT | 10 | | |
| US-09-215-649A-12 | | | |
| Sequence 12, Application US/09215649A | | | |
| Patent No. 6271349 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Anderson, Dirk M. | | | |
| Galibert, Laurent | | | |
| Marasovsky, Eugene | | | |
| TITLE OF INVENTION: Receptor Activator of NF-kappaB | | | |
| NUMBER OF SEQUENCES: 19 | | | |
| CORRESPONDENCE ADDRESSES: | | | |
| ADDRESSEE: Immunex Corporation, Law Department | | | |
| STREET: 51 University Street | | | |
| CITY: Seattle | | | |
| STATE: WA | | | |
| COUNTRY: USA | | | |
| ZIP: 98101 | | | |
| COMPUTER READABLE FORM: | | | |
| MEDIUM TYPE: Floppy disk | | | |
| COMPUTER: Apple Power Macintosh | | | |
| OPERATING SYSTEM: Apple Operating System 7.5.5 | | | |
| SOFTWARE: Microsoft Word for Power Macintosh 6.0.1 | | | |
| CURRENT APPLICATION DATA: | | | |
| APPLICATION NUMBER: US/09/215,649A | | | |
| FILING DATE: 17-Dec-1998 | | | |
| CLASSIFICATION: <Unknown> | | | |
| PRIOR APPLICATION DATA: | | | |
| APPLICATION NUMBER: 08/996,139 | | | |
| FILING DATE: <Unknown> | | | |
| APPLICATION NUMBER: USN 08/813,509 | | | |
| FILING DATE: 07 MARCH 1997 | | | |
| APPLICATION NUMBER: USSN 08/772,330 | | | |

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1 FILING DATE: 23 DECEMBER 1996
2
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Perkins, Patricia Anne
5 REGISTRATION NUMBER: 34,693
6 REFERENCE/DOCKET NUMBER: 2851-A
7
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (206)587-0430
10 TELEFAX: (206)233-0644
11
12 INFORMATION FOR SEQ ID NO: 12:
13
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 954 base pairs
16 TYPE: nucleic acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: cDNA
20 HYPOTHEICAL: NO
21 ANTI-SENSE: NO
22 ORIGINAL SOURCE:
23 ORGANISM: Homo sapiens
24 IMMEDIATE SOURCE:
25 LIBRARY: <unknown>
26 CLONE: hURANKL (full length)
27
28 FEATURE:
29 NAME/KEY: CDS
30 LOCATION: 1..951
31
32 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
33
34 US-09-215-649A-12
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US-08-584-031-2
Sequence 2, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 1042
TYPE: DNA
ORGANISM: Homo sapiens
US-08-584-031-2

Query Match 3.6%; Score 58.4; DB 3; Length 1042;
Best Local Similarity 50.0%; Pred. No. 1.9e-06;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 525 AACATGACGTTAAGCAACGAAACTAAGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
DB 586 aacttgcaacttgagatgagtgacgtgcacatcgaagaaagggttactacatctat 645
QY 585 GCCAACATTGCTTTGGCATCATGAACATCGGAGCGTACTACGACTATCTTCA 644
DB 646 tcccaaacatcttgcattcctcagagaa---ataaagaataaaccaagaacgacaaa 702
QY 645 CTGATGCTGATGCTGTTAAACCAACATCAAAATCCCAAGTTCTATTACCTGTATGAAA 704
DB 703 caaatggtccaaatatcttcaataacacaaagttacccctcatttgatgaa 762
QY 705 GGAGGAGCAGCAAAAACCTGTCGGCAATTCGAATTCCTCAATTCATTAATGTT 764
DB 763 agtgcagagaatagtgctgctcgaagtgagaaatgagctctatcctcatalcaaa 822
QY 765 GGGGATTTTTCAGCTCCGACCTGTGAGAAATTAGCATTCAGCTGCCAACCTTCC 824
DB 823 gggggaattttgagctcgaagaaatgagaaatcttctcgtcgaacaaatgagcac 882
QY 825 CTGCTGATCCGATCAAGATCGACGTAATTCGAGCTTGGGCTTCAAGTT 872
DB 883 ttgatagacatgacatgagcagcagcttcttcggggccttctttagt 930

RESULT 14
US-08-780-496-2

Sequence 2, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntcharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-780-496-2

Query Match 3.6%; Score 58.4; DB 3; Length 1042;
Best Local Similarity 50.0%; Pred. No. 1.9e-06;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 525 AACATGACGTTAAGCAACGAAACTAAGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
DB 586 AACTTGCACTTGAGGAATGTAAGTGCATCCATGAAAAAGGTTTACTACATCTAT 645
QY 585 GCCAACATTGCTTTGGCATCATGAACATCGGAGCGTACTACGACTATCTTCA 644
DB 646 TCCCAACATCTTTCGATTTCAGAGGAA---ATTAAGAAACACAAAGAACGACAAA 702
QY 645 CTGATGCTGATGCTGTTAAACCAACATCAAAATCCCAAGTTCTCATTAAGTATGAAA 704
DB 703 CAAATGGCCAAATATATTTCAATACACAAGTATCTCAACCTATATTTGATGAAA 762
QY 705 GGAGGAGCAGCAAAAACCTGTCGGCAATTCGAATTCACACTTTTATTCATAAATGTT 764
DB 763 AGTCTGAAATTAATTTGTTGCTTAAGATGCAAAATATGACTCTATTCATCTATCAA 822
QY 765 GGGGATTTTTCAGCTCCGACCTGTGAGAAATTAGCATTCAGGTCGCCAACCTTCC 824
DB 823 GGGGGAATTTTGAAGCTTAAGAAATGACAGAAATTTTGTCTGTAACAAATGACAC 882
QY 825 CTGCTGATCCGATCAAGATCGACGTAATTCGAGCTTGGGCTTCAAGTT 872
DB 883 TTGATGACATGAGACATGAAAGCAGTTTTCGGGGCCTTTTACTT 930

RESULT 15
US-08-670-354-3

Sequence 3, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HuAIC-0V
FEATURE:
NAME/KEY: CDS
LOCATION: 78..383
US-08-670-354-3

Query Match 3.6%; Score 58.4; DB 1; Length 1521;
Best Local Similarity 50.0%; Pred. No. 2.3e-06;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;
QY 525 AACATGACGTTAGACGAAACTAAGGTTAACCAAGATGGCTTCTATTACTGTAC 584
DB 425 AACTTGACACTTGAGGAATGTGTAAGTGCATCCATGAAAGGGTTTACTACATCTAT 484
QY 585 GCCACATTTGCTTGGGCAATCATGAACATCGGGAAGCTACTACAGACTATCTTCAG 644
DB 485 TCCCAACATACCTTGCATTTCAGAGGAA--ATAAAGAAACACAAAGAACGACAAA 541
QY 645 CTGATGCTATGTCGTTAAACCAAGATCAAAATCCCAAGTCTCATTAACCTGATGAAA 704
DB 542 CAATGCTCCAAATATATTACAAATACACAAGTATTCGACCTATATGTGATGAAA 601
QY 705 GGAAGGACGACGAAAACTGTCGGGCAATTCGAATTCACCTTTATTCATTAATGTT 764
DB 602 AGTCTAGAAATAGTTGTGTAAAGATGCAAAATATGACTCTATTCATCTATCAA 661
QY 765 GGGGGAATTTTCAAGCTCCGAGCTGCTGAGAGAAATAGCATTCAGGTGCCAACCTTCG 824
DB 662 GGGGGAATATTTGAGCTTAAGGAAATGACAGAAATTTTGTCTGTAAACAAATGAGCAC 721
QY 825 CTGCTGATCCGATCAAGATGCGACGTAATTCGGGCTTCAAAAGTT 872
DB 722 TTGATAGCATGACACGAAAGCAGTTTTCGGGGCCTTTTAGTT 769

Search completed: July 8, 2002, 20:04:31
Job time: 710 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 20:04:46 : Search time 2842.81 seconds
(without alignments)
7738.835 Million cell updates/sec

Title: US-09-865-363-10

Perfect score: 1630
1 CCGCGCTCCACACGAGGT.....TAACCTTAATAGACTCTTCAG 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_estlum:*
3: em_estlu:*
4: em_estlu:*
5: em_estlu:*
6: em_estlu:*
7: em_estlu:*
8: em_hic:*
9: gb_estl:*
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11: gb_hic:*
12: gb_hic:*
13: em_gse_hum:*
14: em_gse_hum:*
15: em_gse_hum:*
16: em_gse_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| C 1 | 506.2 | 31.1 | 612 | 12 BH267783 | BH267783 CH230-186 |
| C 2 | 442.4 | 27.1 | 469 | 9 BB223942 | BB223942 BB223942 |
| C 3 | 441 | 27.1 | 475 | 9 BB637568 | BB637568 BB637568 |
| C 4 | 317 | 19.4 | 482 | 10 BB633100 | BB633100 uv73804.Y |
| C 5 | 317 | 19.4 | 514 | 10 BE335979 | BE335979 us84609.Y |
| C 6 | 262.6 | 16.1 | 524 | 12 AQ827122 | AQ827122 HS_5256.B |
| C 7 | 247.8 | 15.2 | 575 | 12 AQ417854 | AQ417854 RPCI-11-1 |
| C 8 | 228.8 | 14.0 | 530 | 9 AA170348 | AA170348 ms88911.F |
| C 9 | 228.4 | 14.0 | 529 | 12 AQ827168 | AQ827168 HS_5256.B |
| C 10 | 205.4 | 12.6 | 659 | 12 AG107545 | AG107545 Pan trogl |
| C 11 | 192 | 11.8 | 419 | 9 AA504450 | AA504450 aa59n12.F |
| C 12 | 181.2 | 11.1 | 362 | 9 AV653073 | AV653073 |
| C 13 | 165.8 | 10.2 | 618 | 12 AZ834036 | AZ834036 2M0116G04 |
| C 14 | 116 | 7.1 | 413 | 12 AQ817650 | AQ817650 HS_5265.B |
| C 15 | 72.2 | 4.4 | 276 | 10 BG203357 | BG203357 RST2738 |
| C 16 | 72.2 | 4.4 | 299 | 10 BG206497 | BG206497 RST25946 |
| C 17 | 70.6 | 4.3 | 277 | 10 BG184205 | BG184205 RST3126.A |

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| C 18 | 70.6 | 4.3 | 609 | 10 BF427340 | BF427340 df64e08.Y |
| C 19 | 69 | 4.2 | 198 | 10 BG197160 | BG197160 RST16397 |
| C 20 | 69 | 4.2 | 321 | 10 BG212237 | BG212237 RST31821 |
| C 21 | 68.4 | 4.2 | 1101 | 12 CNS00FMC | AL070972 Drosophila |
| C 22 | 61 | 3.7 | 683 | 10 BG016736 | BG016736 df64e08.x |
| C 23 | 60 | 3.7 | 1101 | 12 CNS00396 | AL063921 Drosophila |
| C 24 | 59.4 | 3.6 | 928 | 12 CNS00DKY | AL071865 Drosophila |
| C 25 | 58.4 | 3.6 | 618 | 9 BE042463 | BE042463 hc22c06.x |
| C 26 | 58.4 | 3.6 | 683 | 9 AW949689 | AW949689 EST361759 |
| C 27 | 58.4 | 3.6 | 718 | 9 AW945165 | AW945165 EST361358 |
| C 28 | 58.4 | 3.6 | 973 | 9 AL347417 | AL347417 AL547417 |
| C 29 | 58.4 | 3.6 | 1055 | 9 AL543620 | AL543620 AL543620 |
| C 30 | 58.4 | 3.6 | 1101 | 12 CNS00EVL | AL069706 Drosophila |
| C 31 | 58.2 | 3.6 | 1203 | 12 CNS015WU | AL106008 Drosophila |
| C 32 | 57.2 | 3.5 | 907 | 10 CNS04PAP | BM358116 CA_Fa000 |
| C 33 | 56.6 | 3.5 | 1184 | 12 CNS04PAP | AL300850 Tetradon |
| C 34 | 56.2 | 3.4 | 1101 | 12 CNS00EVL | AL069847 Drosophila |
| C 35 | 56 | 3.4 | 775 | 10 BG216814 | BG216814 RST36509 |
| C 36 | 55.6 | 3.4 | 524 | 12 CNS01090 | AL167541 Tetradon |
| C 37 | 55.6 | 3.4 | 647 | 10 BM440311 | BM440311 p91n.pk0 |
| C 38 | 55.4 | 3.4 | 976 | 12 CNS04F5M | AL286627 Tetradon |
| C 39 | 54.6 | 3.3 | 945 | 12 CNS04DOK | AL285149 Tetradon |
| C 40 | 54.2 | 3.3 | 606 | 10 BG112984 | BG112984 p91n.pk0 |
| C 41 | 54.2 | 3.3 | 1101 | 12 CNS00KAE | AL077628 Drosophila |
| C 42 | 54 | 3.3 | 862 | 12 CNS029ER | AL187164 Tetradon |
| C 43 | 54 | 3.3 | 988 | 12 CNS0072R | AL066743 Drosophila |
| C 44 | 54 | 3.3 | 1063 | 12 CNS07A2Y | AL436064 T3 end of |
| C 45 | 53.8 | 3.3 | 585 | 9 AM104819 | AM104819 x057b10.x |

ALIGNMENTS

RESULT 1
LOCUS BH267783/c 612 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-186C1, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH267783
VERSION CH230-186C1, DNA sequence.
KEYWORDS BH267783.1 GI:17180093
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 612)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 EcORI segment
COMMENT Unpublished (1999)
Other_GSSs: CH230-186C1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@tigr.org).
Clones may be purchased from BACPC Resources
(http://www.chori.org/bacpac/or_eirng_inform.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 186 row: C column: 1
Seq primer: T7
Class: BAC ends.
Location/Qualifiers

FEATURES
source 1..612
/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"


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RESULT 9
A0827168/c 529 bp DNA linear GSS 27-AUG-1999
DEFINITION HS_52556_B2_G09_T7A_RPCT-11 Human Male BAC Library Homo sapiens
ACCESSION A0827168
VERSION A0827168.1 GI:5793230
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 529)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCT-11. For BAC
library availability, please contact Pletzer de Jong
(pletzer@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering-bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.hbnc.washington.edu
Plate: 832 row: N column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 529.
Location/Qualifiers
1..529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-832 Col-18 Row-N"
/clone_1lb="RPCT-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI.
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"
BASE COUNT 147 a 121 c 102 g 153 t 6 others
ORIGIN
Query Match 14.0%; Score 228.4; DB 12; Length 529;
Best Local Similarity 72.7%; Pred. No. 1,1e-37;
Matches 336; Conservative 0; Mismatches 115; Indels 11; Gaps 3;

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Db 287 TTGGGGCTTTAAAGTTGAGATATAGATTGAGCCCGAGTTTGGAGTGT---ATGTA 231
Oy 916 TGTCTAGATGTTTGGAAACCTTTCTTAAAA-----ATGATGATGCTATACATGCT 968
Db 230 TCTCTGATGTTTGGAAACATTTTTTNNACAGCCAGAAAGATGTATAGTGTGT 171
Oy 969 AAGACTAAGAGAGAGAGCCCGCCAGCGTGTATGAACATCACAGCCCTCTCTGAGCCT 1028
Db 170 GAGACTACTAAGAGAGAGAGCCCGCCAGCGTGTATGAACATCACAGCTCAGATCAGTCTGAGCCT 111
Oy 1029 GTACAGGTTGTATATATTAAGTCCATAGTGTATGATTCATGTGCT-ATTACACAA 1087
Db 110 GTAGAGAACACGAGATTTTACAGCCAGTGGAGGAGATGTAGCTCATGTGTGTACACAA 51
Oy 1088 CGGTTTACATTTTGTATGATTTTCTTACAGATTTGACCA 1129
Db 50 TGTCTTGTAGATTGTGTAGAGAGTACTAAGACATGTCACACAA 9

RESULT 10
AG107545 659 bp. DNA linear GSS 03-NOV-2001
LOCUS AG107545
DEFINITION Pan troglodytes DNA, clone: PTB-112609.F, genomic survey sequence.
ACCESSION AG107545
VERSION AG107545.1 GI:16728063
KEYWORDS GSS; GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphoblast DNA, clone_1lb:PTB Chimpanzee Male
BAC library clone:PTB-112609.F.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (sites)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 659)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC):
1-7-22 Suehiro-Chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbese@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RAD process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..659
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-112609.F"
/sex="male"
/cell_type="lymphoblast"
/clone_1lb="PTB Chimpanzee Male BAC Library"
BASE COUNT 181 a 168 c 121 g 189 t
ORIGIN
Query Match 12.6%; Score 205.4; DB 12; Length 659;
Best Local Similarity 86.3%; Pred. No. 7.7e-33;
Matches 227; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```


QY 515 CAGATCTCTAATGACGCTTAAAGGAAAGTAAAGGCTTACCAAGATGCTTCTA 574
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 456 CAGATCTCTAATGACGCTTAAAGGAAAGTAAAGGCTTACCAAGATGCTTCTA 515
 QY 575 TTACCTGTACGCGCAATTTGCTTGGCATCATGAAACATCGGGAAGCTTACCTACAGA 634
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 516 TTACCTGTACGCGCAATTTGCTTGGCATCATGAAACATCGGGAAGCTTACCTACAGA 575
 QY 635 CTATCTTACGCTATGCTGTATGCTTTAAACACGATCAAAATCCCAAGTCTCTATA 694
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 576 ATATCTTCAACTATGTGTGACCTACTAAACACGATCAAAATCCCAAGTCTCTATAC 635
 QY 695 CCTGTGAAGAGGAGGACACGA 717
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
 Db 636 CCTGTGAAGAGGAGGACACCA 658

RESULT 11

AA504450 419 bp mRNA linear EST 18-AUG-1997
 LOCUS aa59h12.f1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:825287 5',
 DEFINITION mRNA sequence.

ACCESSION AA504450
 VERSION AA504450.1 GI:2240610
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 419)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonalido, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/RLNL at:
 www-bio.llnl.gov/bdnp/image/image.html
 Seq primer: -28m13 rev1 Et from Amersham
 High quality sequence stop: 400.

FEATURES

source

1. 419
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand CDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGACGCGCGCCGCAATTTTCTTTTCTTTT-3'
]. Double-stranded CDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonalido."

BASE COUNT 121 a 58 c 96 g 144 t
 ORIGIN

Query Match 11.8%; Score 192; DB 9; Length 419;
 Best Local Similarity 73.3%; Pred. No. 4, 7e-30; Indels 22; Gaps 5;
 Matches 321; Conservative 0; Mismatches 95;

QY 1013 CCTCTCTCTGAGCGCTGTAGAGTGTGTATGTAAAGTCCATAGGTGATTTAGATTC 1072
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 4 CCAAGCTCTTGACCTTGTACAGAACACGCGATATTTCAGCCAGTGGAGATGTAGACTC 63
 QY 1073 ATGGTATTCACAGACGGTTTACAAATTTTGTAAATGATTTTCAGATTTGAACACAGTTG 1132
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 64 ATGGTGTTAACAAAGTGTATTTAAATTTGTAAATGATTTTCAGATTTGAACACAGTTG 123
 QY 1133 GGAGAGTATTCGATTCCTTATGAAACCTTACACGAGTCTTGAAGAGGGGTACAGT 1192
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 124 GAGCAATTCAGCGGTGTGACCTATGACAACTGCAATGAGTGGACCTATGAGAGGG- 175
 QY 1193 CTCTGGGCTTACCCCGAGCATGTGCCACCTGAGAACCTTGAATTAAGAGATGCCATG 1252
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 176 -----TTGGTCCCTGGTCATGTGCGCCCTGCGACG -TGAAGTGAGAGGGGTGTCATC 226
 QY 1253 TCATTGCAAGAAATGATGTGAGGGTTAACTTTTGAATTTTACATTTGCGCTG 1312
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 227 T-AGCGCAATTTGAAGATTCATCTGAAGGGCAATTTCTTTGAATTTTACATCATCTG 285
 QY 1313 GGACCTGCAATTAAGTCTTTTCTTAAGCAGAGAGAAATATATGATTTTATAT 1372
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 286 GAACCTGCAAAAAA--TACTTTTCTTAAGAGAGAG-AAAATATATGATTTTATAT 341
 QY 1373 AATGCTAAAGTATATTTAGTGTATGTTTCTGTGCAAACTTTGTAATTAATATAT 1432
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 342 AATATCTTAAGTATATTTTCAGATGATATTTCTTTCGAAAGATATTTGAATTAATAT 401
 QY 1433 TGTCTATAGTATTTGAT 1450
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 402 TGTGCTATAGTATTTGAT 419

RESULT 12
 AV653073 362 bp mRNA linear EST 15-JAN-2002
 LOCUS AV653073 GLC Homo sapiens CDNA clone GLCDB01 3', mRNA sequence.
 DEFINITION AV653073
 ACCESSION AV653073.1 GI:9874087
 VERSION AV653073.1 GI:9874087
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 362)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL Contact: Zeguang Han
 MEDLINE Chinese National Human Genome Center at Shanghai
 COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel.: 86-21-50801919(ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

source

1. 362
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="GLCDB01"
 /tissue_type="corresponding non cancerous liver tissue"

Location/Qualifiers
 1. 362
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="GLCDB01"
 /tissue_type="corresponding non cancerous liver tissue"


```
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      102 a      80 c      78 g      100 t      2 others
ORIGIN
```

```
Query Match      11.1%; Score 181.2; DB 9; Length 362;
Best Local Similarity 71.3%; Pred. No. 8.4e-28;
Matches 296; Conservative 0; Mismatches 59; Indels 60; Gaps 2;
```

```
QY 131 CGCTCTGTTCTGTTACTTTGAGGCGAGATGATCTTAACAGATATCAGACAGACAC 190
Db 1 CGCCCTGTTCTTCTATTTCAGAGCGGAGATGATCTTAATAGATATTCAGAAATATGCGAC 60
QY 191 TCACCTGTTTATATGATCTGAGACTCCATGAAAGCGAGATTTGAGAGCTCGACTCT 250
Db 61 TCACCTGATTTATATGATTTTGAAGACTCCATGAAATGCGAGATTTTCAGACACAACTCT 120
QY 251 GGAGAGTGAAGACAC-----ACTACCTGACTCTGTCAGAGAGATGAACAGCCCTTCA 304
Db 121 GGAGAGTCAAGATATCAAAATTAATACCTGATTCATGAGAGATTAACAGAGCCCTTCA 180
QY 305 GGGGGCGCTGCAGAGAACTGCAACACATTTGGGGCCACAGCGCTTCTCAGAGACTCC 364
Db 181 AGAGAGTGTCTC----- 191
QY 365 AGCTATGATGAGAGCGTCAATGTTGGATGTCGCCAGCGCAAGCCCTGAGCCACGCC 424
Db 192 -----TGGTGATGCTCATGTTAGATCTGGCCAGAGAGAGCGCAAGCTTGAAGCTCAGCC 246
QY 425 ATTTGACACACTTCACCATCAATGCTGCCAGCATCCCATGGGTTCCATTAAGTCACTCT 484
Db 247 TTTTGGTCATCTCATCTATTAATGTCACCGACATCCCATCTGCTGCCATTAAGTGAAGTCT 306
QY 485 GTTCCTTGGTACGACGATCGAGCGGCGCAAGATCTCTAATCAGTACGCTTAAGC 539
Db 307 GTCTCTTGGTACATGATCGGNGTTGGGCCAAGATCTTCCACATGACTTTTAAAGC 361
```

```
RESULT 13
A2834036      618 bp      DNA      linear      GSS 20-FEB-2001
LOCUS      2M0116G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC2M0116G04 R, DNA sequence.
ACCESSION      A2834036
VERSION      A2834036.1 GI:13003944
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingy,A., von Niederhausen,A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
```

```
JOURNAL
COMMENT      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0116 row: G column: 04
Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends
```

```
FEATURES
source      High quality sequence stop: 618.
Location/Qualifiers
1..618
```

```
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0116G04"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-."
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114bp/AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
BASE COUNT      160 a      163 c      130 g      165 t
ORIGIN
```

```
Query Match      10.2%; Score 165.8; DB 12; Length 618;
Best Local Similarity 96.0%; Pred. No. 1.5e-24;
Matches 170; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 147 TTTGAGCGGAGATGATCTCTAATCAGATATTCAGAAAGACGACCTAGCTCTTTATAGA 206
Db 26 TTCCCTCTGTAGATGATCTCTAATCAGATATTCAGAAAGACGACCTAGCTCTTTATAGA 85
QY 207 ATCTGAGACTCATGAAAGCGAGATTTGACAGACTCGACTGAGAGTGAAGACACA 266
Db 86 ATCTGAGACTCATGAAAGCGAGATTTGACAGACTCGACTGAGAGTGAAGACACA 145
QY 267 CTACCTGACTCTGACGAGAGATGAACAAGCTTTACAGGGGCGCTGCAGAGCAA 323
Db 146 CTACCTGACTCTGACGAGAGATGAACAAGCTTTACAGGGGCGCTGCAGAGCAA 202
```

```
RESULT 14
A0817650      413 bp      DNA      linear      GSS 26-AUG-1999
LOCUS      HS_5265.B1.D03-SP6E RPT-11 Human Male BAC Library Homo sapiens
DEFINITION      genomic clone Plate=841 Col=5 Row=H, DNA sequence.
ACCESSION      A0817650
VERSION      A0817650.1 GI:5780043
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
```

```
REFERENCE
AUTHORS      Kellar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
JOURNAL
MEDLINE      93380589
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
```

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end web server: http://www.htsc.washington.edu

Plate: 841 row: H column: 5
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 413.
Location/Qualifiers

FEATURES

source

1. 413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate841 Col-5 Row-H"
/clone_lib="RPCI-11 Human Male BAC library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

BASE COUNT 108 a 82 c 100 g 123 t
ORIGIN

Query Match 7.1%; Score 116; DB 12; Length 413;
Best Local Similarity 69.9%; Pred. No. 4e-14; Indels 4; Gaps 1;
Matches 172; Conservative 0; Mismatches 70;

OY 733 ATCTGCAATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGCTCCGAGCTGGG 792
|||||
DB 3 ATCTGCAATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGCTCCGAGCTGGG 62
OY 793 AAGAAATTAAGCATGAGTGTCAACCTTCCTGCTGATCCGATCAAGATCGACGT 852
|||||
DB 63 AGGAATTCATCATGAGGTCTCCACCCCTCTACTGATGCCGATCAAGATCGACAT 122
OY 853 ACTTTGGGGCTTCAAGTTCAAGTATGAGTATGATGATCTATTCCTGGAACATTAGCAT 912
|||||
DB 123 ACTTTGGGGCTTCTTAAGACGAGATATGATGATGATGATGATGATGATGATGAT 178
OY 913 GGAATGCTAGATGTTGAACCTCTTAATAAATGATGATGATGATGATGATGATGAT 972
|||||
DB 179 TGTATTCCTGATTTGCGAACAATTTTAACACGCGAGCTAGATGATGATGATGATGAT 238
OY 973 CTACTA 978
|||||
DB 239 CTACTA 244

RESULT 15
BG203357/c 276 bp mRNA linear EST 21-APR-2001
LOCUS BG203357
DEFINITION RST22738 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG203357
VERSION BG203357.1 GI:13725044
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 276)
Harrington, J. J., Sherif, B., Rundlett, S., Jackson, P. D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
E., Veloso, N., Kliska, A., Hess, J., Colhen, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.

TITLE
Creation of genome-wide protein expression libraries using random

JOURNAL
MEDLINE
21227151
COMMENT
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atherys.com
High quality sequence stop: 276.
Location/Qualifiers

FEATURES

source

1. 276
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Atherys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 92 a 51 c 59 g 74 t
ORIGIN

Query Match 4.4%; Score 72.2; DB 10; Length 276;
Best Local Similarity 78.9%; Pred. No. 5.7e-05;
Matches 86; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 359 AGCTCCAGCTATGATGAGGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 418
|||||
DB 114 ATCTCCAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 55
OY 419 CCAGCATTTTGCACACCTCACCATCAATGCTGCCAGACGATCCGAGGT 467
|||||
DB 54 TCAGCTTTGCTCATCTCACTATTAATGCGCCGACGATCCATCTGCT 6

Search completed: July 8, 2002, 22:30:54
Job time: 8768 sec

THIS PAGE BLANK (USPTO)

PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells
 XX
 PS Claim 27; Pages 55-57; 80pp; English.

CC This represents a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

XX Sequence 294 AA:

Query Match 100.0%; Score 1561; DB 19; Length 294;
 Best Local Similarity 100.0%; Pred. No. 2,4e-140;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVPHEGPIHPAPAPAPAPPAASRMFLALIGLGGOVCSIALFLYFRKQMPNRISE 60
 DB 1 gvphegplhpapapapppaasrmflaliglggvcsialfllyfrqmpnrise 60
 QY 61 DSTHCFYRLIRHENADLQDSTLESDTLPSCRMKAFOGAVOKETOHITVGPORFSGA 120
 DB 61 dsthcfyrlirhenadlqdstlesedtlpscrmkafgavoketohivgporfsga 120
 QY 121 PAMEGSWLDVAORGKPEAOPFAHLTINAAISIPSGSHKVTLSWYHDKGMAKISMTLSN 180
 DB 121 pamegswldvaorgkpeaopfahltnaasipsghkvtlsswyhdkgwakismtln 180
 QY 181 GKLRVNDGFFYLYANICFRHHEGSGVPTDYLQIMVYVVKTSIKIPSSHNMKGSGTKN 240
 DB 181 gklrvndgffylyanicfrhhegsvptdyqlimvyvvtksikipshnmkgsgstkn 240
 QY 241 WSGNSEFHYSINVGFFELRAGEEISIQVSNPSLIDPDODATYFGARFVODID 294
 DB 241 wsgnsefhysinvgffelrageeislqvsnpslldpdodatyfgarfvgid 294

RESULT 2

AAW68292 standard; Protein: 294 AA.

AC AAW68292;
 DT 08-OCT-1998 (first entry)
 DE NF-kB receptor activator RANK ligand (RANKL).

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

OS Mus musculus.
 XX
 PN W09828424-A2.
 XX
 PD 02-JUL-1998.

XX 22-DEC-1997; 97MO-US23866.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

PA (IMMV) IMMUNEX CORP.

PI Anderson DM, Galibert LJ, Maraskovsky E;

DR N-PSDB: AAV41371.

XX NPI: 1998-377655/32.

PT New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 55-57; 80pp; English.

CC This represents a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 294 AA:

Query Match 100.0%; Score 1561; DB 19; Length 294;
 Best Local Similarity 100.0%; Pred. No. 2,4e-140;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVPHEGPIHPAPAPAPPAASRMFLALIGLGGOVCSIALFLYFRKQMPNRISE 60
 DB 1 gvphegplhpapapapppaasrmflaliglggvcsialfllyfrqmpnrise 60
 QY 61 DSTHCFYRLIRHENADLQDSTLESDTLPSCRMKAFOGAVOKETOHITVGPORFSGA 120
 DB 61 dsthcfyrlirhenadlqdstlesedtlpscrmkafgavoketohivgporfsga 120
 QY 121 PAMEGSWLDVAORGKPEAOPFAHLTINAAISIPSGSHKVTLSWYHDKGMAKISMTLSN 180
 DB 121 pamegswldvaorgkpeaopfahltnaasipsghkvtlsswyhdkgwakismtln 180
 QY 181 GKLRVNDGFFYLYANICFRHHEGSGVPTDYLQIMVYVVKTSIKIPSSHNMKGSGTKN 240
 DB 181 gklrvndgffylyanicfrhhegsvptdyqlimvyvvtksikipshnmkgsgstkn 240
 QY 241 WSGNSEFHYSINVGFFELRAGEEISIQVSNPSLIDPDODATYFGARFVODID 294
 DB 241 wsgnsefhysinvgffelrageeislqvsnpslldpdodatyfgarfvgid 294

RESULT 3

AAE08737 standard; Protein: 294 AA.

AC AAE08737;

DT 15-NOV-2001 (first entry)

DE Murine receptor activator of NF kappaB ligand (RANKL) protein.

| | | | | | |
|-----------------------|---|--------------------|-------------|-------------|-------------|
| XX | Murine: receptor activator of nuclear factor kappaB ligand; RANKL; NF- | 100.0% | Score 1561; | DB 22; | Length 294; |
| KW | tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; | 100.0% | | | |
| KW | immune response; inflammatory response; graft-versus-host reaction; | 100.0% | | | |
| KW | toxic shock; sepsis; acute inflammatory reaction; bone resorption; | 100.0% | | | |
| XX | anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory. | 100.0% | | | |
| OS | Mus musculus. | 100.0% | | | |
| PN | US6271349-B1. | 100.0% | | | |
| PD | 07-AUG-2001. | 100.0% | | | |
| XX | | 100.0% | | | |
| PF | 17-DEC-1998; 98US-0215649. | 100.0% | | | |
| XX | | 100.0% | | | |
| PR | 23-DEC-1996; 96US-0059978. | 100.0% | | | |
| PR | 07-MAR-1997; 97US-0077181. | 100.0% | | | |
| PR | 14-OCT-1997; 97US-0064671. | 100.0% | | | |
| PR | 23-DEC-1996; 96US-0772230. | 100.0% | | | |
| PR | 07-MAR-1997; 97US-0813509. | 100.0% | | | |
| PR | 22-DEC-1997; 97US-0996139. | 100.0% | | | |
| XX | | 100.0% | | | |
| PA | (IMNV) IMMUNEX CORP. | 100.0% | | | |
| PI | | 100.0% | | | |
| PI | Dougall WC, Galibert L; | 100.0% | | | |
| XX | | 100.0% | | | |
| DR | WPI: 2001-520313/57. | 100.0% | | | |
| DR | N-PDB: AAD15310. | 100.0% | | | |
| XX | | 100.0% | | | |
| PT | New receptor activator of NF-kappaB (RANK) polypeptides, useful for | 100.0% | | | |
| PT | regulating immune response, in screening for RANK inhibitors, or as an | 100.0% | | | |
| PT | adjunct therapy for disease characterized by neoplastic cells that | 100.0% | | | |
| XX | express RANK - | 100.0% | | | |
| PS | Example 15; Column 65-68; 47pp; English. | 100.0% | | | |
| XX | | 100.0% | | | |
| CC | The patent discloses novel receptor activator of nuclear factor (NF)- | 100.0% | | | |
| CC | kappaB (RANK) proteins and their corresponding DNAs. RANK is a member | 100.0% | | | |
| CC | of the tumour necrosis factor (TNF) receptor superfamily and associates | 100.0% | | | |
| CC | with TNF receptor associated factor (TRAF) 2 and 3 which are important | 100.0% | | | |
| CC | in the regulation of immune and inflammatory response. The receptors | 100.0% | | | |
| CC | are useful for regulating immune response and in screening for inhibitors | 100.0% | | | |
| CC | of these receptors. The cytoplasmic domain of RANK is used in developing | 100.0% | | | |
| CC | assays for inhibitors of signal transduction, e.g. for screening the | 100.0% | | | |
| CC | molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, | 100.0% | | | |
| CC | TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists | 100.0% | | | |
| CC | are useful in ameliorating the negative effects of an inflammatory | 100.0% | | | |
| CC | response that result from triggering of RANK, e.g. in treating toxic | 100.0% | | | |
| CC | shock or sepsis, graft-versus-host reactions, acute inflammatory | 100.0% | | | |
| CC | reactions and the effects of bone resorption. RANK acts as an anti- | 100.0% | | | |
| CC | apoptotic signal and rescue the cells that express RANK from apoptosis. | 100.0% | | | |
| CC | Soluble forms of the receptor are used in vivo or in vitro based | 100.0% | | | |
| CC | screening tests for agonists or antagonists of RANK activity, as | 100.0% | | | |
| CC | antagonists of RANK-mediated NF-kappa B activation, or to inhibit | 100.0% | | | |
| CC | transduction of a signal via RANK. RANK compositions are used in the | 100.0% | | | |
| CC | development of both agonistic and antagonistic antibodies, or as an | 100.0% | | | |
| CC | adjunct therapy for disease characterised by neoplastic cells that | 100.0% | | | |
| CC | express RANK. Compounds that interfere with RANK/TRAF6 interactions | 100.0% | | | |
| CC | are useful for modulating the formation of osteoclasts from osteoclast | 100.0% | | | |
| CC | precursors and for modulating osteoclast function and activities. They | 100.0% | | | |
| CC | are used as inhibitors of diseases associated with excess bone resorption | 100.0% | | | |
| CC | and as immunosuppressants or anti-inflammatory agents. The RANK DNAs | 100.0% | | | |
| CC | are useful for the expression of recombinant proteins, as probes for analysis | 100.0% | | | |
| CC | of the presence or distribution of RANK transcripts, while the proteins | 100.0% | | | |
| CC | are useful in preparing kits for the detection of soluble RANK, or | 100.0% | | | |
| CC | monitor RANK-related activity. The present sequence is RANK ligand | 100.0% | | | |
| CC | (RANKL) protein from murine. | 100.0% | | | |
| XX | | 100.0% | | | |
| XX | | 100.0% | | | |
| Sequence | 294 AA; | 100.0% | | | |
| Query Match | 100.0%; | Score 1561; | DB 22; | Length 294; | |
| Best Local Similarity | 100.0%; | Pred No. 2,4e-140; | | | |

| Matches | 294; Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps |
|-----------|-------------------------------------|---|-------------|---|--------|----|------|
| Qy | 1 | GVPHGELHPA | PSAPAPAPPAA | SRSMFTLLGLGLGVVCSIALFLYRAQMDPNRISE | 60 | | |
| Db | 1 | gvphegrph | pepsapapapp | paasrsmfllalglglgvvcsialflftraqmdpnrlse | 60 | | |
| Qy | 61 | DSTHCFFRIIL | RLHNAADLOD | STLESEPTLLPDSGRKKAKAFQGVQVKELOHIYGPQRFSA | 120 | | |
| Db | 61 | dstchcfrilr | lhnaadldst | lesedclpdserrmkqafqsgvqkelhlyvgpqrfsga | 120 | | |
| Qy | 121 | PAMNEGSLDVA | QGRKEPEAO | PFALHTITNAASIPSGSHKVTLSWSYHDRGMAKISNMTLSN | 180 | | |
| Db | 121 | pamnegswld | vaqgrkpeaq | pfahltitnaasipsgshkvrltswyhdrgmakismntlsn | 180 | | |
| Qy | 181 | GKLKLVNDG | FYLYLYANIC | CFRHNETSGSPVDYQLWLVYVVKTSIKIPSHNLMGSGSTKN | 240 | | |
| Db | 181 | gklklyndgd | fylylyanalc | frhnetsgsvpcdyqlwlvyyvktalkipsashnlmgsgstkn | 240 | | |
| Qy | 241 | MSGNSEPFHS | INVGGFKL | RAGEISIOVSNPSLLDPDDATYEGAFYQDID | 294 | | |
| Db | 241 | wsgnsefhs | invggfklr | ageisiovsnpsslldpddatylgafrvqdid | 294 | | |
| RESULT 4 | | | | | | | |
| AAE04425 | AAE04425 standard; Protein; 294 AA. | | | | | | |
| AAE04425: | | | | | | | |
| XX | AC | | | | | | |
| XX | DT | 04-SEP-2001 (first entry) | | | | | |
| XX | DE | Murine receptor activator of NF- κ B ligand (RANKL) protein. | | | | | |
| XX | MM | Murine: receptor activator of NF- κ B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein. | | | | | |
| XX | OS | Mus musculus. | | | | | |
| XX | XX | | | | | | |
| XX | FH | Key | | | | | |
| XX | FT | Region | | | | | |
| XX | FT | Location/Qualifiers | | | | | |
| XX | XX | 139..294 | | | | | |
| XX | XX | /note="Receptor binding region" | | | | | |
| XX | XX | US6242213-B1. | | | | | |
| XX | PD | 05-JUN-2001. | | | | | |
| XX | PE | 22-DEC-1997; 97US-0995659. | | | | | |
| XX | PR | 23-DEC-1996; 96US-0059978. | | | | | |
| XX | PR | 07-MAR-1997; 97US-0077181. | | | | | |
| XX | PR | 14-OCT-1997; 97US-0064671. | | | | | |
| XX | PA | (IMMV) IMMUNEX CORP. | | | | | |
| XX | PI | Anderson DM; | | | | | |
| XX | XX | | | | | | |
| DR | DR | WPI; 2001-407216/43. | | | | | |
| XX | DR | N-PDB; AAD08714. | | | | | |
| XX | PT | New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF- κ B receptor activator) of the receptor activator of NF- κ B (RANK) | | | | | |
| XX | PS | Example 7; Column 59-62; 43pp; English. | | | | | |
| CC | CC | The present invention relates to receptor activator of NF- κ B (RANK) | | | | | |
| CC | CC | DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF. The DNA molecules are useful for producing ligands of RANK | | | | | |

CC The ligands are useful for regulating immune response and in screening
XX for inhibitors of RANK. The present sequence is murine RANKL protein.
50 Sequence 294 AA;

| | | | | |
|---------------------------|---------|---------------------|--------|-------------|
| Query Match | 100.0% | Score 1561; | DB 22; | Length 294; |
| Best Local Similarity | 100.0%; | Pred. No. 2,4e+140; | | |
| Matches 294; Conservative | 0; | Mismatches | 0; | Gaps 0 |

QY 1 GVPHEGPLHAPSA^PA^PAP^PPAASRSMFLALIGLGQVVCISIAFLYFRAQMDPNRISE 60
|||||
|||||
|||||
Db 1 gvphegplhapapsapapppaasrsmflaliglgqvvcisialflyfraqm^dpnrise 60

QY 61 DSTHCFYRLILHENADLQDSTLESEDTLPDSCHRMKQAFOGAVOKELQHTVGPQRHSGA 1200
|||||
|||
Db 61 dsthcfyrrllrhenadlqdstlesedtlpdschrmkgfvgavkqlghvqpqrtsga 1200

QY 121 PAMGEGSWLDVAQRGRPEAQFAHLTTAAASIPSGSHKVTLLSSWYHDRGNAKISNNLTLSN 180

Db 121 pammegswldraqgrpeaqfahlttinaasipsgshkvllsswyhdrgwakisnmtlsn 180

```
QY 181 GKLRYNDGEFYLYANICFRHHETSGSPYDYLQMLVYVWKTSLKIPSSHNMKGSGSTKN 240C
|||||
|||||
|||||
Db 181 gklrYnqdgfYlyan:cfrhEtsGspYtdYlqMlvYvWktsIkIpsShNmKgsGstKn 240C
```

QY 241 WSCNSEFHFFSINVGFFKRLRAGEELISIQVSNPSLDDPDQATYFGAFKRVQDID 294
 |||||
 DB 241 wsgnsefhfysinvgffkrlrageelisqvsnpslldpdqatylfgafkqvqid 294

| RESULT | 5 |
|------------------------------------|---|
| AAE01992 | |
| AAE01992 standard. Protein: 204 AA | |

| | | |
|----|-------------|---------------|
| XX | AAE01992; | |
| AC | | |
| XX | | |
| DT | 31-JUN-2001 | (first entry) |

XX Murine RANKL (receptor activator of NF-kappaB ligand) protein.
DE
XX
XX Mouse: receptor activator of NF-kappaB. RANK: nuclear factor-k

KM NF-kappab; tumour necrosis factor; TNF; type1 transmembrane protein;
KM TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
KM inflammatory reaction; bone resorption; gene therapy; immunomodulator;
KM immune system dysfunction; familial expansile osteolysis; FEO;

| | |
|----|--|
| KM | early onset Paget's disease of bone; EP; cytostatic. |
| XX | |
| OS | Mus musculus. |
| XX | |

| | |
|----|--------------|
| PN | WO200136637- |
| XX | |
| PD | 25-MAY-2001. |
| XX | |

| | | |
|----|--------------|-----------------|
| PF | 14-NOV-2000; | 2000WO-US31459. |
| XX | | |
| PR | 17-NOV-1999; | 99US-0442029. |
| XX | | |

PA (IMMV) IMMUNEX CORP
XX
PI Anderson DM, Hughes
XX

| | |
|----|---------------------|
| PT | New DNA encoding a |
| XX | |
| DR | N-PSDB; AAD05903. |
| DR | WPI; 2001-329222/34 |

PT treatment of Paget's disease and family
XX
XX Disclosure; Page 74-75; 96pp; English
PS
XX

aa The present invention relates to a novel receptor, referred to as RANK
cc (receptor activator of NF (nuclear factor)- κ pab), a member of TNF
cc (tumour necrosis factor) receptor superfamily. RANK is a Type I

transmembrane protein that interacts with TNF receptor-associated factors (TRAFs). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation of the transcription factor NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system. Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNMs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset Paget's disease of bone (EP). The present amino acid sequence is murine RANKL (murRANKL) protein.

| AA | Sequence | 294 AA |
|----|----------|--------|
| SQ | | |

| | | | | |
|---------------------------|---------|---------------------|--------|-------------|
| Query Match | 100.0% | Score 1561; | DB 22; | Length 294; |
| Best Local Similarity | 100.0%; | Pred. No. 2.4e-140; | | |
| Matches 294; Conservative | 0; | Mismatches | 0; | Gaps 0 |

QY 1 GVPHEGLHPAPSA PAPAPPPAASBSMFLALIGLGLGVCSIALFLYPRRAQMDPKRISE 60C

Db 1 gvphegplhpapsa papappppaasbsmflaliglgvgvcsialfllyfraqmdpkprise 60C

```
QY      61 DSTHCFYRLRHNADLDSTSEEDTLPDSCRMMKQAFQGAVOKELQHTVGPQRFSGA   120
        |||
Db       61 dsthcfyrlrhnadldstsesedtlpdscrmkgatfgavqkelqlhvpgqrfsqa   120
```

```

Oy 121 PAMMEGSLDVAQRGKEPAQFPAHLTTAAASIPSGSHKVTLSWHDGRGAKISNMTLN 180
      |||||
Db 121 pammegswldvargkpeaqfahltlnaasipsgshkvtlsswyhdrgvakismtltn 180

```

[illegible][illegible]

RESULT 6
AAW83194
ID AAW83194 standard. Protein. 316 AA

```

XX
AC      AAW83194;
XX
DE      11-EBB-1000 (first entry)

```

| XX | Human osteoprotegerin binding protein from the 32D-F3 ins |
|----|---|
| DE | |
| XX | Human osteoprotegerin binding protein: OPG binding protei |
| XX | |

KW osteoporosis; osteoclast maturation; bone disease; metastasis; OAR;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
KW Paget's disease.
VY
VY

| | |
|----|--------------|
| OS | Homo sapiens |
| XX | |
| PN | W09846751-A1 |
| XY | |

| | |
|----|----------------------------|
| PD | 22-OCT-1998. |
| XX | |
| PF | 15-APR-1998; 98WO-US07584. |
| XY | |

| | | |
|----|--------------|--------------|
| XX | | |
| PR | 30-MAR-1998; | 98US-0052521 |
| PR | 16-APR-1997; | 97US-0842842 |
| PR | 23-JUN-1997; | 97US-0880855 |

PR 23-JUN-1997; 9/

XX

PA (AMGE-) AMGEN INC

| | | |
|----|--------------------|--------------|
| PR | 10-APR-1991; | 9705-0842042 |
| PR | 23-JUN-1997; | 9705-0880855 |
| XX | | |
| PA | (AMGE-) AMGEN INC. | |

SECRET (TOP SECRET)

XX Boyle WJ:
XX
XX WPI: 1998-594578/50.
DR N-PSDB: AAV70284.
XX
PT Nucleic acid encoding osteoprotegerin binding protein - useful for
PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
XX
PS Claim 19: Fig 1: 47pp: English.
XX
CC The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegerin (OPG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
XX
SQ Sequence 316 AA:

Query Match 99.6%; Score 1554; DB 19: Length 316;
Best Local Similarity 99.7%; Pred. No. 1.2e-139;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVPHGEPHAPAPAPAPAPAPASRSNMFLLGLGQVCSIALFLYFRAMDPNRIS 60
DB 23 gvphegplhpapapapapapapasmflla1191919qvcstall1lyfraqmdpnriise 82
OY 61 DSTHCFYRILRLHENDLSDSTLESEDTLPDSCRRKQAFQAVQKELQIHYGPQRFSGA 120
DB 83 dsthcfyrlrlhenaagldgstlesedtlpdsctrmkqfagvqkelqihlyvqprfsga 142
OY 121 PAMMEGSMLDVAORGRPEAPFAHLITINASTIPSGSHKVTLSWYHGRWAKTSNMTLSN 180
DB 143 pammeqswldvaqrgrpeapfahlltinaas1psgshkvltswyhdrgwaktsnmclsn 202
OY 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWVYVVKTSIKIPSSHNLKMGSGSTKN 240
DB 203 gklrvngdgfyylyanlcfhhetsgsvptdyqlmwvvyvvtksiklpsshnlmkgsctkn 262
OY 241 WSGNSEFHYSINWGFYFKLRAGEEISIQVNSPLDPPDQATYFGAFKQODID 294
DB 263 wsgnsefhyslnwgfkykrlageeelsiqvnsplldppdqatylfgafkvqddid 316

RESULT 7
ID AAM83017 standard; Protein: 316 AA.
XX
AC AAM83017;
XX
DT 10-FEB-1999 (first entry)
XX
DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
XX
KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW osteoclast; bone absorption factor; bone disorder; calcium metabolism.
XX

OS Unidentified.
XX
XX PN WO9846644-A1.
XX
XX PD 22-OCT-1998.
XX
XX PE 15-APR-1998; 98WO-JP01728.
XX
XX PR 02-DEC-1997; 97JP-0332241.
XX PR 15-APR-1997; 97JP-0097808.
XX PR 09-JUN-1997; 97JP-0151434.
XX PR 12-AUG-1997; 97JP-0217897.
XX PR 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Hiasashio K, Kinoshita M, Kobayashi F, Morinaga T;
XX Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
XX Washida N, Yamaguchi K, Yano K, Yasuda H;
DR WPI: 1998-594563/50.
DR N-PSDB: AAV69886.
XX
PT Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism
XX
PS Claim 8: Pages 106-108; 151pp; Japanese.
XX
CC The present sequence represents an osteoclastogenesis inhibitory factor
CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC separation and maturation of osteoclasts in the presence of bone
CC absorption factors such as calcitriol or parathyroid hormone (PTH).
CC OBM is isolated from stroma cells cultured in the presence of a bone
CC absorption factor by separation and solubilisation of membrane proteins
CC then affinity chromatography using OCIF. It exists in a full-sequence
CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
CC used for screening potential inhibitors and modifiers of its biological
CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
CC components of drugs.
XX
SQ Sequence 316 AA:

Query Match 99.6%; Score 1554; DB 19: Length 316;
Best Local Similarity 99.7%; Pred. No. 1.2e-139;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVPHGEPHAPAPAPAPAPAPASRSNMFLLGLGQVCSIALFLYFRAMDPNRIS 60
DB 23 gvphegplhpapapapapapapasmflla1191919qvcstall1lyfraqmdpnriise 82
OY 61 DSTHCFYRILRLHENDLSDSTLESEDTLPDSCRRKQAFQAVQKELQIHYGPQRFSGA 120
DB 83 dsthcfyrlrlhenaagldgstlesedtlpdsctrmkqfagvqkelqihlyvqprfsga 142
OY 121 PAMMEGSMLDVAORGRPEAPFAHLITINASTIPSGSHKVTLSWYHGRWAKTSNMTLSN 180
DB 143 pammeqswldvaqrgrpeapfahlltinaas1psgshkvltswyhdrgwaktsnmclsn 202
OY 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWVYVVKTSIKIPSSHNLKMGSGSTKN 240
DB 203 gklrvngdgfyylyanlcfhhetsgsvptdyqlmwvvyvvtksiklpsshnlmkgsctkn 262
OY 241 WSGNSEFHYSINWGFYFKLRAGEEISIQVNSPLDPPDQATYFGAFKQODID 294
DB 263 wsgnsefhyslnwgfkykrlageeelsiqvnsplldppdqatylfgafkvqddid 316

RESULT 8

Tue Jul 9 13:21:00 2002

us-09-865-363-11.rag

Page 11

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 8, 2002, 18:51:11 ; Search time 52.39 Seconds
(Without alignments)
137.071 Million cell updates/sec

Title: US-09-865-363-11

Perfect score: 1561
Sequence: 1 GVPHGGLHPPASAPAPAP.....LLDPDQATYFGAFKVVQID 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 1561 | 100.0 | 294 | 3 | US-08-996-139-11 |
| 2 | 1561 | 100.0 | 294 | 4 | US-08-995-659-11 |
| 3 | 1561 | 100.0 | 294 | 4 | US-09-215-649A-11 |
| 4 | 1554 | 99.6 | 316 | 2 | US-08-842-842-7 |
| 5 | 1554 | 99.6 | 316 | 4 | US-08-989-362-2 |
| 6 | 1554 | 99.6 | 316 | 4 | US-09-052-521C-2 |
| 7 | 1326.5 | 85.0 | 317 | 3 | US-08-996-139-13 |
| 8 | 1326.5 | 85.0 | 317 | 4 | US-08-995-659-13 |
| 9 | 1326.5 | 85.0 | 317 | 4 | US-09-215-649A-13 |
| 10 | 1326.5 | 85.0 | 317 | 4 | US-09-052-521C-4 |
| 11 | 258.5 | 16.6 | 279 | 4 | US-09-072-993C-3 |
| 12 | 258.5 | 16.6 | 281 | 1 | US-08-670-354-2 |
| 13 | 258.5 | 16.6 | 281 | 3 | US-08-584-031-1 |
| 14 | 258.5 | 16.6 | 281 | 3 | US-08-780-496-1 |
| 15 | 258.5 | 16.6 | 281 | 4 | US-08-883-086-10 |
| 16 | 258.5 | 16.6 | 281 | 4 | US-09-320-424-2 |
| 17 | 258.5 | 16.6 | 281 | 4 | US-09-333-593A-6 |
| 18 | 258.5 | 16.6 | 281 | 5 | PCT-US96-10895-2 |
| 19 | 251 | 16.1 | 291 | 1 | US-08-670-354-6 |
| 20 | 251 | 16.1 | 291 | 5 | PCT-US96-10895-6 |
| 21 | 251 | 16.1 | 291 | 5 | PCT-US96-10895-6 |
| 22 | 239 | 15.3 | 286 | 4 | US-09-320-424-13 |
| 23 | 239 | 15.3 | 286 | 4 | US-09-320-424-13 |
| 24 | 229.5 | 15.1 | 273 | 4 | US-09-105-343A-7 |
| 25 | 224 | 14.3 | 183 | 4 | US-09-105-343A-8 |
| 26 | 177.5 | 11.4 | 278 | 4 | US-08-339-214-16 |
| 27 | 177.5 | 11.4 | 278 | 4 | US-08-339-214-16 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 177 | 11.3 | 279 | 4 | US-08-339-214-24 | Sequence 24, App1 |
| 29 | 177 | 11.3 | 279 | 4 | US-08-339-214-32 | Sequence 32, App1 |
| 30 | 174 | 11.1 | 281 | 4 | US-08-810-453-2 | Sequence 2, App1 |
| 31 | 174 | 11.1 | 281 | 3 | US-08-815-190A-2 | Sequence 2, App1 |
| 32 | 174 | 11.1 | 281 | 4 | US-09-290-640-25 | Sequence 25, App1 |
| 33 | 174 | 11.1 | 281 | 4 | US-09-479-524-3 | Sequence 3, App1 |
| 34 | 174 | 11.1 | 281 | 4 | US-08-339-214-8 | Sequence 8, App1 |
| 35 | 174 | 11.1 | 281 | 4 | US-08-339-214-30 | Sequence 30, App1 |
| 36 | 174 | 11.1 | 281 | 5 | PCT-US95-00362-2 | Sequence 2, App1 |
| 37 | 169.5 | 10.9 | 261 | 1 | US-07-940-605A-2 | Sequence 2, App1 |
| 38 | 169.5 | 10.9 | 261 | 1 | US-08-184-422-8 | Sequence 8, App1 |
| 39 | 169.5 | 10.9 | 261 | 1 | US-08-360-923A-2 | Sequence 2, App1 |
| 40 | 169.5 | 10.9 | 261 | 1 | US-08-446-922-4 | Sequence 4, App1 |
| 41 | 169.5 | 10.9 | 261 | 2 | US-08-431-055-4 | Sequence 4, App1 |
| 42 | 169.5 | 10.9 | 261 | 2 | US-08-690-096-2 | Sequence 2, App1 |
| 43 | 169.5 | 10.9 | 261 | 2 | US-08-249-189-12 | Sequence 12, App1 |
| 44 | 169.5 | 10.9 | 261 | 2 | US-08-484-624A-12 | Sequence 12, App1 |
| 45 | 169.5 | 10.9 | 261 | 2 | US-08-477-733B-12 | Sequence 12, App1 |

ALIGNMENTS

RESULT 1
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-11

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Query Match          100.0%; Score 1561; DB 3; Length 294;
Best Local Similarity 100.0%; Pred. No. 2,8e-153;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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| QY | 1 | GVPHEGPLHAPASAPAPAPPAPASMSMLALLGLIGOVCSIALFLYFRAOMDPNRIS | 60 |
| | | | |
| Db | 1 | GVPHEGPLHAPASAPAPAPPAPASMSMLALLGLIGOVCSIALFLYFRAOMDPNRIS | 60 |
| QY | 61 | DSTHCFYILRLHNEADLQDSTLSEBDPLPDCSRMKQAFQGAOKELOHIVGPOFSGA | 120 |
| | | | |
| Db | 61 | DSTHCFYILRLHNEADLQDSTLSEBDPLPDCSRMKQAFQGAOKELOHIVGPOFSGA | 120 |
| QY | 121 | PAMMGSMULDVAQORCKPEAPQFAHTITNAASIPSGSHKVTLSWYHDROGMAKISNMTLSN | 180 |
| | | | |
| Db | 121 | PAMMGSMULDVAQORCKPEAPQFAHTITNAASIPSGSHKVTLSWYHDROGMAKISNMTLSN | 180 |
| QY | 181 | GKLRYNODGFYLYLVANICFRHHTSGSVPTDYLQLMVYVVKTSIKIPSSHNLMMKGSTGN | 240 |
| | | | |
| Db | 181 | GKLRYNODGFYLYLVANICFRHHTSGSVPTDYLQLMVYVVKTSIKIPSSHNLMMKGSTGN | 240 |
| QY | 241 | WSGNEEFHFYTSINNCGFETKRGCESTIOVNSPLDPPDQATYFCAFVQDID | 294 |
| | | | |
| Db | 241 | WSGNEEFHFYTSINNCGFETKRGCESTIOVNSPLDPPDQATYFCAFVQDID | 294 |

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RESULT      2
US-08-995-659-11
: Sequence 11, Application US/08995659
: Patent No. 6242213
: GENERAL INFORMATION:
:   APPLICANT: Anderson, Dirk M.
:   APPLICANT: Galibert, Laurent
:   APPLICANT: Maraskovsky, Eugene
:   TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
:   NUMBER OF SEQUENCES: 19
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Immunex Corporation, Law Department
:     STREET: 51 University Street
:     CITY: Seattle
:     STATE: WA
:     COUNTRY: USA
:     ZIP: 98101
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: Apple Power Macintosh
:     OPERATING SYSTEM: Apple Operating System 7.5.5
:     SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/995, 659
:     FILING DATE: 22 DECEMBER 1997
:   CLASSIFICATION:
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: USSN 60/064, 671
:       FILING DATE: 14 OCTOBER 1997
:     CLASSIFICATION:
:       PRIOR APPLICATION DATA:
:         APPLICATION NUMBER: USSN 08/813, 509
:         FILING DATE: 07 MARCH 1997
:     CLASSIFICATION:
:       PRIOR APPLICATION DATA:
:         APPLICATION NUMBER: USSN 08/772, 330
:         FILING DATE: 23 DECEMBER 1996
:     CLASSIFICATION:
:       ATTORNEY/AGENT INFORMATION:
:         NAME: Perkins, Patricia Anne
:         REGISTRATION NUMBER: 34, 693
:         REFERENCE/DOCKET NUMBER: 2852-A
:         TELECOMMUNICATION INFORMATION:
:           TELEPHONE: (206)587-0430
:           TELEFAX: (206)233-0644
:     INFORMATION FOR SEQ ID NO: 11:
:       SEQUENCE CHARACTERISTICS:

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1      LENGTH      294 amino acids
2      TYPE: amino acid
3      TOPOLOGY: linear
4      MOLECULE TYPE: protein
5      US-08-995-659-11
6
7      Query Match      100.0%; Score 1561; DB 4; Length 294;
8      Best Local Similarity 100.0%; Pred. No. 2,8e-153;
9      Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
10
11      QY      1      GVPHEGPIHPAPSAAPAPPPAPASMSMLLALIGLGVCSIALFLYFRKQMPNRISE 60
12      DB      1      GVPHEGPIHPAPSAAPAPPPAPASMSMLLALIGLGVCSIALFLYFRKQMPNRISE 60
13      QY      61      DSTHCFYILRLRHEVADLQDSTLESEDTLPDSCRMKQAFQAVOKELQHIYGPQRFSGA 120
14      DB      61      DSTHCFYILRLRHEVADLQDSTLESEDTLPDSCRMKQAFQAVOKELQHIYGPQRFSGA 120
15      QY      121     PAMMGSMILDVANQKRPAPQPPAHLITINAASIPSGSKHYTLSSWYHDRGMAKISMWTLN 180
16      DB      121     PAMMGSMILDVANQKRPAPQPPAHLITINAASIPSGSKHYTLSSWYHDRGMAKISMWTLN 180
17      QY      181     GKLARNQGGFYLYLVNICEFRHETSGSVPTDLOLVYVVKISIKIPSSHNLMKGGSTKN 240
18      DB      181     GKLARNQGGFYLYLVNICEFRHETSGSVPTDLOLVYVVKISIKIPSSHNLMKGGSTKN 240
19      QY      241     WSGNSEFPHYSINVGGFELKLRAGEEISIQVSNPSLLDPDQATYGAERKVID 294
20      DB      241     WSGNSEFPHYSINVGGFELKLRAGEEISIQVSNPSLLDPDQATYGAERKVID 294
21
22      RESULT      3
23      US-09-215-649A-11
24      : Sequence 11, Application US/09215649A
25      : Patent No. 6271349
26      : GENERAL INFORMATION:
27      : APPLICANT: Anderson, Dirk M.
28      : Galibert, Laurent
29      : Markskovsky, Eugene
30      : TITLE OF INVENTION: Receptor Activator of NF-kappaB
31      : NUMBER OF SEQUENCES: 19
32      : CORRESPONDENCE ADDRESSES:
33      : ADDRESS: Immunex Corporation, Law Department
34      : STREET: 51 University Street
35      : CITY: Seattle
36      : STATE: WA
37      : COUNTRY: USA
38      : ZIP: 98101
39      : COMPUTER READABLE FORM:
40      : MEDIUM TYPE: floppy disk
41      : COMPUTER: Apple Power Macintosh
42      : OPERATING SYSTEM: Apple Operating System 7.5.5
43      : SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
44      : CURRENT APPLICATION DATA:
45      : APPLICATION NUMBER: US/09/215,649A
46      : FILING DATE: 17-Dec-1998
47      : CLASSIFICATION: <Unknown>
48      : PRIOR APPLICATION DATA:
49      : APPLICATION NUMBER: 08/996,139
50      : FILING DATE: <Unknown>
51      : APPLICATION NUMBER: USSN 08/813,509
52      : FILING DATE: 07 MARCH 1997
53      : APPLICATION NUMBER: USSN 08/772,330
54      : FILING DATE: 23 DECEMBER 1996
55      : ATTORNEY/AGENT INFORMATION:
56      : NAME: Perkins, Patricia Anne
57      : REGISTRATION NUMBER: 34,693
58      : REFERENCE/DOCKET NUMBER: 2851-A
59      : TELECOMMUNICATION INFORMATION:
60      : TELEPHONE: (206)587-0430
61      : TELEFAX: (206)233-0644
62      : INFORMATION FOR SEQ ID NO: 11:

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SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match 100.0%; Score 1561; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 2,8e-153;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVPHEGRLHAPASAPAPAPPAASRSMFLALLGLGIGVCSIALFLYFRAMPNRISE 60
DB 1 GVPHEGRLHAPASAPAPPAASRSMFLALLGLGIGVCSIALFLYFRAMPNRISE 60
QY 61 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMRKQAFQAVOKELQHVGPORFSGA 120
DB 61 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMRKQAFQAVOKELQHVGPORFSGA 120
QY 121 PAMMEGSLDVAQKRPAPAPFAHLTTNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 180
DB 121 PAMMEGSLDVAQKRPAPAPFAHLTTNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 180
QY 181 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 240
DB 181 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 240
QY 241 WSGNSEFFHYSINVGGFFKLRAGEEISTOVSNPSILDDPDODATYFGAFKVDID 294
DB 241 WSGNSEFFHYSINVGGFFKLRAGEEISTOVSNPSILDDPDODATYFGAFKVDID 294

RESULT 4
US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-842-842-7

Query Match 99.6%; Score 1554; DB 2; Length 316;
Best Local Similarity 99.7%; Pred. No. 1,7e-152;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVPHEGRLHAPASAPAPPAASRSMFLALLGLGIGVCSIALFLYFRAMPNRISE 60
DB 23 GVPHEGRLHAPASAPAPPAASRSMFLALLGLGIGVCSIALFLYFRAMPNRISE 82
QY 61 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMRKQAFQAVOKELQHVGPORFSGA 120
DB 83 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMRKQAFQAVOKELQHVGPORFSGA 142
QY 121 PAMMEGSLDVAQKRPAPAPFAHLTTNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 180
DB 143 PAMMEGSLDVAQKRPAPAPFAHLTTNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 202
QY 181 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 240
DB 203 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 262
QY 241 WSGNSEFFHYSINVGGFFKLRAGEEISTOVSNPSILDDPDODATYFGAFKVDID 294
DB 263 WSGNSEFFHYSINVGGFFKLRAGEEISTOVSNPSILDDPDODATYFGAFKVDID 316

RESULT 5
US-08-989-362-2
Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-362-2

Query Match 99.6%; Score 1554; DB 4; Length 316;
Best Local Similarity 99.7%; Pred. No. 1,7e-152;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GVPHEGRLHAPASAPAPPAASRSMFLALLGLGIGVCSIALFLYFRAMPNRISE 60
|||||

Db 23 GVPHEGPIHPAPAPAPAPAPAPASMSMFLALLGLGIGVCSIALFLYFRAMPDNRISE 82
QY 61 DSTHCFYRLRLRHENADLQDSTLESEDTLPDSCRMMKQAFQGAQVQKELQHIYVGPORFSGA 120
Db 83 DSTHCFYRLRLRHENAGLQDSTLESEDTLPDSCRMMKQAFQGAQVQKELQHIYVGPORFSGA 142
QY 121 PAMMEGSMIDVAQGRKPEAOPFAHLITINAASIPSGSHKVTLSWYHNRGAKISNMTLN 180
Db 143 PAMMEGSMIDVAQGRKPEAOPFAHLITINAASIPSGSHKVTLSWYHNRGAKISNMTLN 202
QY 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWYVYKTSIKIPSSHNLKMGSGSTKN 240
Db 203 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWYVYKTSIKIPSSHNLKMGSGSTKN 262
QY 241 WSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDDATYFGAFKQVODID 294
Db 263 WSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDDATYFGAFKQVODID 316

RESULT 6
US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451BIV
; CURRENT APPLICATION NUMBER: US/09/052, 521C
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880, 855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842, 842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mouse
US-09-052-521C-2

Query Match 99.6%; Score 1554; DB 4; Length 316;
Best Local Similarity 99.7%; Pred. No. 1.7e-152;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GVPHEGPIHPAPAPAPAPAPAPASMSMFLALLGLGIGVCSIALFLYFRAMPDNRISE 60
Db 23 GVPHEGPIHPAPAPAPAPAPAPASMSMFLALLGLGIGVCSIALFLYFRAMPDNRISE 82
QY 61 DSTHCFYRLRLRHENADLQDSTLESEDTLPDSCRMMKQAFQGAQVQKELQHIYVGPORFSGA 120
Db 83 DSTHCFYRLRLRHENAGLQDSTLESEDTLPDSCRMMKQAFQGAQVQKELQHIYVGPORFSGA 142
QY 121 PAMMEGSMIDVAQGRKPEAOPFAHLITINAASIPSGSHKVTLSWYHNRGAKISNMTLN 180
Db 143 PAMMEGSMIDVAQGRKPEAOPFAHLITINAASIPSGSHKVTLSWYHNRGAKISNMTLN 202
QY 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWYVYKTSIKIPSSHNLKMGSGSTKN 240
Db 203 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWYVYKTSIKIPSSHNLKMGSGSTKN 262
QY 241 WSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDDATYFGAFKQVODID 294
Db 263 WSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDDATYFGAFKQVODID 316

RESULT 7
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.

APPLICANT: Gallibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996, 139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064, 671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813, 509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772, 330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13

Query Match 85.0%; Score 1326.5; DB 3; Length 317;
Best Local Similarity 84.5%; Pred. No. 5.4e-129;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;
QY 1 GVPHEGPIHPAPAPAPAPAPAPASMSMFLALLGLGIGVCSIALFLYFRAMPDNRISE 60
Db 23 GVPHEGPIHPAPAPAPAPAPAPASMSMFLALLGLGIGVCSIALFLYFRAMPDNRISE 81
QY 61 DSTHCFYRLRLRHENADLQDSTLESEDTLPDSCRMMKQAFQGAQVQKELQHIYVGPORFSGA 118
Db 82 DSTHCFYRLRLRHENAGLQDSTLESEDTLPDSCRMMKQAFQGAQVQKELQHIYVGPORFSGA 141
QY 119 GAPAMMEGSMIDVAQGRKPEAOPFAHLITINAASIPSGSHKVTLSWYHNRGAKISNMTLN 178
Db 142 AKAAMMEGSMIDVAQGRKPEAOPFAHLITINAASIPSGSHKVTLSWYHNRGAKISNMTLN 201
QY 179 SNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWYVYKTSIKIPSSHNLKMGSGST 238
Db 202 SNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWYVYKTSIKIPSSHNLKMGSGST 261
QY 239 KWSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDDATYFGAFKQVODID 294
Db 262 KWSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDDATYFGAFKQVODID 317

RESULT 8
US-08-995-659-13
; Sequence 13, Application US/08995659

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-2

Query Match 16.6%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 1,1e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

OY 21 PAASRMFLALGLGQVCSIALFLYFRAQMD--PNRISEDSTHCFYRIILRHENADL 78
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKGIACF-----LKEDDSY 64
OY 79 QDSTLESDTLPSDCRKMKAFOGAVOK-----ELQHIYGPQRSGAPAMM 124
DB 65 WDP--NDEESMNSPCWQVKMQLRQLVRKMLRTSEETISTVOEKQONISPL----- 113
OY 125 EGSWLDVAQRKPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GMAKIS 174
DB 114 -----VREGRQRYA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
OY 175 NMTLSNGKLAVNODGFYLYANICFRHNETSGSVPTDYQLAMVYVVKTSIKIPSSHNLK 234
DB 166 NLHNRNGELVIEHKGFFYYSQTYFRQEEIKENTKNDKQWQYIYKYT--SYDPDILLK 224
OY 235 GGSTKNMNGSEFHFYSINVGFFKLAGEEISIQVSNPSLDDODDQATYFGAKV 290
DB 225 SARNSCWSKDAEYGLSTYOGGIFELKENDRIEVSVTNEHLIDMDHASFAGFLV 280

RESULT 13
US-08-584-031-1
Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584, 031A
CURRENT FILING DATE: 1996-01-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 16.6%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1,1e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

OY 21 PAASRMFLALGLGQVCSIALFLYFRAQMD--PNRISEDSTHCFYRIILRHENADL 78
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKGIACF-----LKEDDSY 64
OY 79 QDSTLESDTLPSDCRKMKAFOGAVOK-----ELQHIYGPQRSGAPAMM 124
DB 65 WDP--NDEESMNSPCWQVKMQLRQLVRKMLRTSEETISTVOEKQONISPL----- 113
OY 125 EGSWLDVAQRKPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GMAKIS 174
DB 114 -----VREGRQRYA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
OY 175 NMTLSNGKLAVNODGFYLYANICFRHNETSGSVPTDYQLAMVYVVKTSIKIPSSHNLK 234
DB 166 NLHNRNGELVIEHKGFFYYSQTYFRQEEIKENTKNDKQWQYIYKYT--SYDPDILLK 224

OY 235 GGSTKNMNGSEFHFYSINVGFFKLAGEEISIQVSNPSLDDODDQATYFGAKV 290
DB 225 SARNSCWSKDAEYGLSTYOGGIFELKENDRIEVSVTNEHLIDMDHASFAGFLV 280

RESULT 14
US-08-780-496-1
Sequence 1, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntcharapai, Kyung Jin Kim
TITLE OF INVENTION: APO-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-780-496-1

Query Match 16.6%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1,1e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

OY 21 PAASRMFLALGLGQVCSIALFLYFRAQMD--PNRISEDSTHCFYRIILRHENADL 78
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKGIACF-----LKEDDSY 64
OY 79 QDSTLESDTLPSDCRKMKAFOGAVOK-----ELQHIYGPQRSGAPAMM 124
DB 65 WDP--NDEESMNSPCWQVKMQLRQLVRKMLRTSEETISTVOEKQONISPL----- 113
OY 125 EGSWLDVAQRKPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GMAKIS 174
DB 114 -----VREGRQRYA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
OY 175 NMTLSNGKLAVNODGFYLYANICFRHNETSGSVPTDYQLAMVYVVKTSIKIPSSHNLK 234
DB 166 NLHNRNGELVIEHKGFFYYSQTYFRQEEIKENTKNDKQWQYIYKYT--SYDPDILLK 224
OY 235 GGSTKNMNGSEFHFYSINVGFFKLAGEEISIQVSNPSLDDODDQATYFGAFV 290
DB 225 SARNSCWSKDAEYGLSTYOGGIFELKENDRIEVSVTNEHLIDMDHASFAGFLV 280

RESULT 15
US-08-883-086-10
Sequence 10, Application US/08883086

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 8, 2002, 18:51:51 ; Search time 62.2 seconds

(without alignments)
454.184 Million cell updates/sec

Title: US-09-865-363-11

Perfect score: 1561
Sequence: 1 GVPHEGRLHPAPSAPAPAPPP.....LLDPDQATYFGAFKVDID 294

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 185.5 | 11.9 | 261 | 2 S53090 | CD40 ligand - bovl |
| 2 | 177.5 | 11.4 | 278 | 2 A49266 | fes ligand - rat |
| 3 | 177 | 11.3 | 279 | 2 A53062 | Fas ligand - mouse |
| 4 | 174 | 11.1 | 281 | 2 I38707 | Fas ligand - human |
| 5 | 169.5 | 10.9 | 261 | 2 I53476 | CD40 ligand - human |
| 6 | 153 | 9.8 | 260 | 2 S21738 | CD40 ligand - mous |
| 7 | 149 | 9.5 | 234 | 1 J01344 | tumor necrosis fac |
| 8 | 146.5 | 9.4 | 235 | 1 QWMSN | tumor necrosis fac |
| 9 | 143.5 | 9.2 | 233 | 1 S22052 | tumor necrosis fac |
| 10 | 141 | 9.0 | 234 | 1 JH0529 | tumor necrosis fac |
| 11 | 140 | 9.0 | 233 | 2 S11688 | tumor necrosis fac |
| 12 | 139.5 | 8.9 | 233 | 1 QWHYN | tumor necrosis fac |
| 13 | 137.5 | 8.8 | 234 | 1 A25451 | tumor necrosis fac |
| 14 | 135.5 | 8.7 | 235 | 2 I54490 | tumor necrosis fac |
| 15 | 133.5 | 8.6 | 233 | 1 S24642 | tumor necrosis fac |
| 16 | 133 | 8.5 | 185 | 2 S52715 | tumor necrosis fac |
| 17 | 133 | 8.5 | 232 | 1 S12606 | tumor necrosis fac |
| 18 | 129.5 | 8.3 | 235 | 2 J00029 | tumor necrosis fac |
| 19 | 129.5 | 8.3 | 306 | 2 I49139 | lymphotoxin-beta |
| 20 | 117 | 7.5 | 244 | 2 A46066 | lymphotoxin beta |
| 21 | 115.5 | 7.4 | 193 | 2 S06192 | tumor necrosis fac |
| 22 | 104.5 | 6.7 | 340 | 2 S49742 | hypothetical prote |
| 23 | 103 | 6.6 | 3848 | 2 T17414 | hypothetical prote |
| 24 | 101 | 6.5 | 440 | 2 I49681 | glyceraldhyde-3-P |
| 25 | 97 | 6.2 | 450 | 2 S38114 | hypothetical prote |
| 26 | 93.5 | 6.0 | 205 | 1 QWHUX | lymphotoxin alpha |
| 27 | 92.5 | 5.9 | 197 | 1 JH0309 | tumor necrosis fac |
| 28 | 90.5 | 5.8 | 750 | 2 E84475 | probable Athlia re |
| 29 | 90 | 5.8 | 1694 | 2 S50065 | sialoadhesin - mou |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 88.5 | 5.7 | 202 | 1 B27303 | tumor necrosis fac |
| 31 | 88.5 | 5.7 | 1547 | 2 J00096 | hypothetical 176k |
| 32 | 88 | 5.6 | 347 | 2 H75253 | hypothetical prote |
| 33 | 88 | 5.6 | 498 | 2 T39005 | hypothetical prote |
| 34 | 87.5 | 5.6 | 868 | 2 A30817 | serendipity (ary h |
| 35 | 87 | 5.6 | 785 | 2 T23456 | hypothetical prote |
| 36 | 85.5 | 5.5 | 558 | 2 T23649 | hypothetical prote |
| 37 | 85.5 | 5.5 | 578 | 2 S51379 | probable phosphoe |
| 38 | 85.5 | 5.5 | 1090 | 2 AG1749 | glycosidase homolo |
| 39 | 85 | 5.4 | 549 | 2 J05926 | secreted Klotho pr |
| 40 | 85 | 5.4 | 639 | 2 A32935 | protein P1 - Entam |
| 41 | 85 | 5.4 | 1012 | 2 J05925 | membrane klotho pr |
| 42 | 84.5 | 5.4 | 202 | 1 JN0869 | tumor necrosis fac |
| 43 | 84 | 5.4 | 317 | 2 E75421 | conserved hypothet |
| 44 | 84 | 5.4 | 451 | 2 T36149 | hypothetical prote |
| 45 | 84 | 5.4 | 658 | 2 T39500 | serine/threonine-s |

ALIGNMENTS

```
RESULT 1
S53090
CD40 ligand - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: S53090
R:Merits: B.E.L.C.: Murliki, M.
submitted to the EMBL Data Library, February 1995
A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A:Reference number: S53090
A:Accession: S53090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <MEM>
A:Cross-references: EMBL:248469; NID:g732569; PIDN:CAA8363.1; PID:g732570

Query Match 11.9% Score 185.5; DB 2; Length 261;
Best local similarity 24.7% Pred. No. 2.9e-08;
Matches 71; Conservative 54; Mismatches 122; Indels 41; Gaps 13;

QY 10 PAPSAPAPPPAASRSMFLALIGLGVCSIALF-LYFRAQMPNRISEDSTICFYR 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 PPSRVATGPP--VSMKIFMYLLTVFLITQMGISALFAVYLLHRLDKIE-DEKRLHEDV 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 69 ILPLHENAQLDSTLSEDTLPDSCRMRKQAFQGAAYOKELQHTVGFQRTSGAPAMMEGSM 128
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 FMKTIORCNKNGEGSLSL-----NCEEIIRSREFDLVKDIMON---KEYKKKKKNFE-- 112
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 129 LDVAQRKPEAOPFAHLITINASIPSGSHKVTLSMYHGRGNAKISN--MTLSNGK-LRV 185
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 113 ---MHGDEPEQIAAHV-----ISEASSKTTSVLQMAPRGYTTLSNNLVTLENGQQLAV 163
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 186 NQDFEYLYANICE-RHNETSGSVPTDYQLMYYVVKTSIKIPSSH--LMKGGSTKNMS 242
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 164 KRQGFYIYQVTFCSNRETLQAP-----FISLKLKSPSGSERLLLAANTH--S 213
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 243 GNEFFHYIINNGFKKLAGEEISIQVSNPSLLDPDQATYFGAFKV 290
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 214 SSRPCGQSIHLGGVPELQSGASVFVNVDPQVSHGTGFTSGTLKL 261
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
A49266
fes ligand - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: A49266
R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A>Title: Molecular cloning and expression of the Fas ligand, a novel member of the tu
A:Reference number: A49266; MUID:94084792
```


Oy 163 SWYHGRGAKNSMTLSNGKRLRVNODGFYUAYLANICFHHNHERSGVPRIDYQLQAWYVYKT 222
 Db 161 EMEDEVYGLVLLSGVAYKKKGGLVINTGLTFYYSKYFFGSCNN-----LPLSKKVTMR 214
 Oy 223 SIKIPSSHNLLKKGSGTKMWSGNSSEFHFYSINVGCFPKLRAGEELSIQVSNPSLDDPDODA 282
 Db 215 NSKYPODLYMME-GKMGSYCTTGCGMMARRSSYLGAFAENLTSDHLVNVNSELVLVFEESO 273
 Oy 283 TYFGAFKV 290
 Db 274 TFFGLYKL 281
 RESULT 5
 153476
 CD40 ligand - human
 N:Alternate names: glycoprotein 39, hCD40-L protein; T-cell antigen gp39; TRAP protein
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence, revision 02-Jul-1996 #text, change 20-Apr-2001
 C:Accession: S28017; JH0793; S26594; S28592; I53476; S25664; S30593
 R:Hollenbaugh, D.; Grosmaire, L.S.; Kallias, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
 EMBO J. 11, 4313-4321, 1992
 A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
 A:Reference number: S28017; MUID:93049181
 A:Accession: S28017
 A:Molecule type: MRNA
 A:Residues: 1-261 <HOL>
 A:Cross-references: EMBL:Z15017; NID:938483; PIDN:CAV78737.1; PID:938484
 R:Spriggs, M.K.; Armitage, R.J.; Stockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
 J. Exp. Med. 176, 1543-1550, 1992
 A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
 A:Reference number: JH0793; MUID:93094757
 A:Accession: JH0793
 A:Molecule type: MRNA
 A:Residues: 1-261 <SPR>
 A:Cross-references: GB:K67878; NID:938411; PIDN:CAA48077.1; PID:938412
 A:Experimental source: peripheral blood T-cell
 R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroccek, R.A.
 Eur. J. Immunol. 22, 3191-3194, 1992
 A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
 A:Reference number: S26694; MUID:93076854
 A:Accession: S26694
 A:Status: preliminary
 A:Molecule type: MRNA
 A:Residues: 1-261 <GRA>
 A:Cross-references: EMBL:X65550; NID:937269; PIDN:CAA8554.1; PID:937270
 R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
 FEBS Lett. 315, 239-246, 1993
 A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
 A:Reference number: S28592; MUID:93138085
 A:Accession: S28592
 A:Molecule type: MRNA
 A:Residues: 1-261 <GAU>
 A:Cross-references: EMBL:L07414; NID:9180123; PIDN:AAA35662.1; PID:9180124
 A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
 C:Genetics:
 A:Gene: GDB:CD40LG; HIGM1; TMD3
 A:Cross-references: GDB:120632; OMIM:308230
 C:Map position: Xq26-Xq28
 C:Keywords: glycoprotein; transmembrane protein
 F:13-44/Domain: transmembrane #status predicted <TM>
 F:45-261/Domain: extracellular #status predicted <EXT>
 F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 10.9%; Score 169.5; DB 2; Length 261;
 Best Local Similarity 25.7%; Pred. No. 6,6e-07;
 Matches 75; Conservative 50; Mismatches 116; Indels 51; Gaps 16;
 Oy 11 APSAPAPAPPPASNSMFLALLGLGLGVGVSIALF-LYFAQNDPNRISDSRHCYRI 69
 Db 9 SPSPAAVGLP--ISKIPMYLLTFVLLITQMGSAFAVLLRRRD--KIEDER----- 57

[illegible]

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis
A:Reference number: J01344; MUID:92084125
A:Accession: J01344
A:Molecule type: DNA
A:Residues: 1-234 <SD>
A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C:Comment: This protein is an important proximal mediator of endotoxemia.
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 79/1; 95/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxic; glycoprotein; lipoprotein; lymphokine; macrophage; mem
E:78-234/Product: tumor necrosis factor alpha #status predicted <TM>
E:19-20/Binding site: myristate (lys) (covalent) #status predicted
F:82/Binding site: carbonylate (Ser) (covalent) #status predicted
F:16-178/Disulfide Bonds: #status predicted

Query Match 9.5%, Score 149; DB 1; Length 234;
Best Local Similarity 24.1%; Pred. No. 3,2e-05;
Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

OY 111 IVGPRFGAPAMMGSMILVAQRK-----PEAQFAHLITMAASIPSGHKVTLSSWY 165
 ::::| | | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 55 VIGPQREQLPMAFQ-STINPLAQLTRSSSRPPSPDKPVAAHYVAN----FOAGCOL---QWL 106

OY 166 HDRGNAKIS-MTSLNGKLRVNODGEFYLYANICRHHETSGSVPTDLOLMVYVKTSI 224
 : : : : : | : : : | : : | : : | : : | : : | : : | : : | : : |
DB 107 SGRNALALLGVKKLINDQNVLPDLGLYLITYGYLFK----GGCGSTHVLLTHITSRLAV 162

OY 225 KIPSSHNLMKG-----GSTKMMSGNSEHFHYSINVGFELKLRAGEISIOVSN 272
 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 163 SYPSKYNNLSAIKSPCHTESPEQAARKP-----YPYVLGGVFLEKGDQSALSIHQ 215

OY 273 PSLLD-PPQDATYFG 286
 || : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 216 PNVLDPAESGOVYFG 230

RESULT 8
OMSMN
tumor necrosis factor alpha precursor - mouse
M:Alternate names: cachectin; TNF alpha
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000
C:Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696
R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A:Reference number: A22908; MUID:86224564
A:Accession: A22908
A:Molecule type: DNA
A:Residues: 1-235 <SH>
A:Cross-references: GB:M20155
B:Biorg. Khim. 13, 701-705, 1987
A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
A:Reference number: S03791; MUID:87298639
A:Accession: S03791
A:Molecule type: DNA
A:Residues: 1-235 <SHA>
A:Cross-references: GB:M8296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A>Note: article in Russian with English abstract
R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necr
A:Reference number: A93679; MUID:88067722
A:Accession: A27303
A:Molecule type: DNA
A:Residues: 1-235 <SEM>
A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68550.1; PID:g54832
R:Pernica, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

```
A>Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor protein p60p  
A.Reference number: A25164; MUID:85296296  
A.Accession: A25164  
A:Molecule type: mRNA  
A.Residues: 1-235 <P>  
R.Czech, K.; Beutler, B.  
J. Biol. Chem. 264, 16256-16260, 1989  
A.Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide result  
A.Reference number: A34251; MUID:89380231  
A.Accession: A34251  
A:Molecule type: protein  
A.Residues: 70-87 <CS>  
R.Capit, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
A>Title: Identification of a common nucleotide sequence in the 3'-untranslated region  
A.Reference number: I59058; MUID:86149365  
A.Accession: I59058  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A.Residues: 1'230,'R',232-235 <RES>  
A.Cross-references: GI:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083  
R.Sherry, B.; Jue, D.W.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A>Title: Characterization of high molecular weight glycosylated forms of murine tumor  
A.Reference number: A3696; MUID:91097531  
A.Accession: A3696  
A:Molecule type: protein  
A.Residues: 80-85,'X','87-99 <SHE>  
C:Genetics:  
A.Introns: 62/3; 81/1, 97/1  
A.Note: The first intron occurs in the 5'-untranslated region  
C:Superfamily: tumor necrosis factor  
E:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m  
F:80-235/Product: tumor necrosis factor #status experimental <Mat>  
F:84/Binding site: myristate (lys) (covalent) #status predicted  
F:86/Binding site: carbonylate (Ser) (covalent) #status predicted  
F:148-179/Disulfide bonds: #status predicted  
  
Query Match          9 4%; Score 146.5; DB 1; Length 235;  
Best Local Similarity    25.6%, Pred.No. 5.2e+05;  
Matches      51; Conservative   36; Mismatches     67; Indels       45; Gaps     11;
```



```

DB      158  RFAVSYQOTKWNLLSAIKSPQORETPEGAAKPFW-----XEPYLGWFOLEKDRDLST 210
OY      269  QVSNPSLDD-PDODATYFEG 286
      ::::1::11::111
DB      211  EIMLPAYLPAFSAESGQVYFEG 229

RESULT  12

OMHUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text-change 08-Dec-2000
C:Accession: A93585; S61531; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrc
A:Reference number: A93585; MUID:86016093
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <END>
A:Cross-references: GB:X02910; GB:X02159; NID:q37209; PIDN:CAA26669.1; PID:q37210
R:Riris, R.J.M.; Bouquelieret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the Nkappab family within a
A:Reference number: S36152; MUID:93272029
A:Accession: S36153
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <RID>
A:Cross-references: EMBL:Z15026; NID:q37211; PIDN:CAA78745.1; PID:q37212
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pennica, D.; Nedwin, G.E.; Haylick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to
A:Reference number: A93351; MUID:85086244
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PENN>
A:Cross-references: GB:X02910; GB:X02159; NID:q37209; PIDN:CAA26669.1; PID:q37210
A:Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloid
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lan, L.S.; Strickler, J.; Van Arsdel, J.N.; AC
Science 228, 149-154, 1985
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', '64-233 <MAN>
A:Cross-references: GB:M10988; NID:q339737; PIDN:AAA61198.1; PID:q339738
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; AC
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A:Reference number: A61478; MUID:88301617
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102;109-119;121-128, 'X', '130-131;142-144, 'X', '146, 'XX', '150-152;159-174;180
R:Marmontou, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A:Reference number: I53311; MUID:86030296
A:Accession: I53311
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <MAN>
A:Cross-references: GB:M6331; NID:q339763; PIDN:AAA36758.1; PID:q339764
A:Experimental source: U-937 cells
R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TKA>

```

R.;D'Alfonso, S.; Richiardi, P.M. Immunogenetics 39, 150-154, 1994
A>Title: A polymorphic variation in a putative regulation box of the TNFA promoter re
A:Reference number: I54522; MUID:94102809
A:Accession: I54522
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-8 <DAL>
A:Cross-references: GB:S68530; NID:9544751
R:Stevenson, F.T.; Hursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A>Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific
A:Reference number: A59163; MUID:93018820
A:Contents: annotation; identification of myristylated lysines
R:Aggarwal, B.B.; Kohr, W.U.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, S.A.; Br
J. Biol. Chem. 260, 2345-2354, 1985
A>Title: Human tumor necrosis factor. Production, purification, and characterization.
A:Reference number: A92511; MUID:65130974
A:Contents: annotation; disulfide bond
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induct
out detriment to normal cells. It can also act synergistically with interferon gamma
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos
ut are produced by different cell types and have different induction kinetics.
C:Genetics:
A:Gene: GDB:TNF; TNFA
A:Cross-references: GDB:I20441; OMIM:191160
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m
F.1-76/Domains: propeptide #status predicted <PRO>
F.77-233/Product: tumor necrosis factor #status experimental <MAT>
F.19_20/Binding site: myristate (Lys) (covalent) #status experimental
F.81/Binding site: carboxylate (Ser) (covalent) (partial) #status experimental
F.145-177/Disulfide bonds: #status experimental

```

Query Match Similarity 8.9%; Score 139.5; DB 1; Length 233;
Best Local Similarity 24.9%; Pred. No. 0.0002;
Matches 48; Conservative 34; Mismatches 76; Indels 35; Gaps 9;

QY      111 IVGPQFSGCAPAMMGSGWIDVAQRK---PEAOPRAHLITINAASPSSHKVTLSSWYHD 167
      ::|||
      55 VIGPQEEFPRDLISLIPLAQAVRSSSRTPPSDKPAHVAVN---PQAEGL--QWLNRR 107
      ::|||
QY      168 RGMATSN-MTLISNGLRPNODGFYLIYANICEFRHETSGSVPTDYLQ-----RWY 218
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      108 RANALLANGVELRDNOLVYPSECLILITYQLFK---GQGPSTHVLLTHTRISIAVSY 163
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      219 VVK---TSIKIPSSHNLMKGGSTKNWSGNSEFHSYINWGGFFKLRAGEISIOVSNPS 274
      ::|||
      164 GPKVNLISAIKSCQRETPEGAEAKPW-----YEPILVGGVFLQEKGRDLSAEINRPD 216
      ::|||
QY      275 LLD-PPQDATFYG 286
      |||
Db      217 YLDFAESGGVYFG 229
      |||

RESULT 13
A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
C:accession: A25454; A25451; U50727
R:Title: H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for
A:Reference number: A25454; MUID:86219711
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <Ito>

```

A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A:Reference number: A25451; MUID:86219712
 A:Accession: A25451
 A:Molecule type: DNA
 A:Residues: 1-234 <172>
 A:Note: This sequence differs from that shown in having a Gln inserted between residues
 R:Shakhov, A.N.; Kuprash, D.V.; Azarov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
 A:Reference number: JH0309; MUID:91065534
 A:Accession: J50727
 A:Molecule type: DNA
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Residues: 1-62, 'Q', 63-234 <SHA>
 A:Cross-references: GB:M60340; GB:M5326; NID:g165754; PIDN:AAA31484.1; PID:g165756
 C:Genetics: 62/3; 80/1; 96/1
 A:Introns: 62/3; 80/1; 96/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem
 F:1-81/Domains: propeptide #status predicted <PRO>
 F:82-234/Product: tumor necrosis factor #status predicted <MAT>
 F:19, 20/Binding site: myristate (lys) (covalent) #status predicted
 F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:147-178/Disulfide bonds: #status predicted

Query Match 8.8%; Score 137.5; DB 1; Length 234;
 Best Local Similarity 22.6%; Pred. No. 0.0003;
 Matches 68; Conservative 31; Mismatches 99; Indels 103; Gaps 12;

OY 5 EEPHAPASAPAPAPASR-----SFWALLGLGLQVWCSIALFLYFRAQMPNRTS 59
 |||||
 DB 14 EEPPL-----PKKAGPGGSKRCILSLFSLVAVATTLC---LHFRVIGQERES 63
 OY 60 EOSTCEFYRLTLHENADLODSTLESDTLPSCKRMQAQVAGAKLOHIVGQRRSG 119
 |||||
 DB 64 PNNLLV-----NPAQAVTLLNS-----ASRAISDKLAHV----- 95
 OY 120 APAMEGSLDVAQRGKPEAPFAHLITMAASIPSGSHKVTLLSYHNRGMAKISN-WTL 178
 |||||
 DB 96 ANPQVEG-----LQWLSRAANALLANGMKL 121
 OY 179 SNGKRVNODGFFLYLANICRHHETSGVPTDYLQLVVYVKTSPKIPSSHNMKG--- 235
 |||||
 DB 122 TDNQLVVPADGLYLYSQVLF-----SCGGRSYVLLTHFVSRAVSPYRNKVNLLSAIKS 176
 OY 236 -----GSKMWSGSEFFHYFYSINVGFFKLRAGEISIOVNSPLD-PPQDATYF 285
 |||||
 DB 177 PCHRETPPEAEPMAM-----YEPYLGAVFQLEKGRLESTVENQPEYLDLAEQGYF 229
 OY 286 G 286
 |||||
 DB 230 G 230

RESULT 14

154490
 Tumor necrosis factor alpha precursor - white-footed mouse
 C:Species: Peromyscus leucopus (white-footed mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
 C:Accession: 154490
 R:Crew, M.D.; Filipowsky, M.E.
 Immunogenetics 35, 351-353, 1992
 A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc
 A:Reference number: 154490; MUID:92218012
 A:Accession: 154490
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-235 <RES>
 A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:
 A:Gene: P1TNF
 A:Introns: 62/3; 81/1; 97/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation
 F:19, 20/Binding site: myristate (lys) (covalent) #status predicted
 F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 8.7%; Score 135.5; DB 2; Length 235;
 Best Local Similarity 25.1%; Pred. No. 0.00045;
 Matches 51; Conservative 31; Mismatches 68; Indels 53; Gaps 10;

OY 111 IVGPORFSGAP-----AMMEGSLDVAQRGKPEAPFAHLITMAASIPSGSHKVTLS 163
 |||||
 DB 55 VIGPQREKFPNNPLITGSMQTLTLRSSQNSSD-KPAHVAN-----HQVDEQL 105
 OY 164 WYHDGMAKISNMTLSNG-KLRVNO-----DGFYVLYLANICFRHHETSGSPDYDQLMV 217
 |||||
 DB 106 EWLNRG-----ANALLANGMDLKDMLVLPADGLVLYSQVLEKQGGSSVY-----LIT 155
 OY 218 YVVK-----TSIKIPSSHNMKGSTKNNSGSEFFHYFYSINVGFFKLRAGE 264
 |||||
 DB 156 HTVSRAVSYEDKYNLLSAIKSPCKREPPESSELKPM-----YEPYLGAVFQLEKGR 208
 OY 265 EISIOVNSPLD-PPQDATYFG 286
 |||||
 DB 209 RLSAEVNLPLKYLDPAESQGYF 231

RESULT 15

1524642
 tumor necrosis factor alpha precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: 146047; S24642
 R:Cludes, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
 Cytokine 5, 336-341, 1993
 A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
 A:Reference number: 146046; MUID:94083525
 A:Accession: 146047
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-233 <CL2>
 A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
 C:Genetics:
 A:Gene: TNFA
 A:Introns: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F:20/Binding site: myristate (lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:145-177/Disulfide bonds: #status predicted

Query Match 8.6%; Score 133.5; DB 1; Length 233;
 Best Local Similarity 25.8%; Pred. No. 0.00066;
 Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

OY 111 IVGPOR--FSGAPAMEGSLDVAQRGKPEA---OPFAHLITMAASIPSGSHKVTLSWY 165
 |||||
 DB 55 VIGPQREESPGGSL--NSPLVQTLTRSSQASNNKVAHVAD-----INSFG 100
 OY 166 HDGMAKISNMTLSNG-KLRVNO-----DGFYVLYLANICFRHH-----ETSGSVP 209
 |||||
 DB 101 QLRWMSYANALMANGVKLEDNQLVVPADGLYLYSQVLFRCQGCPSPTPLFTHTISRA 160
 OY 210 TDYQLMAYVYVTSIKIPSSHNMKGSTKNNSGSEFFHYFYSINVGFFKLRAGEISIQ 269
 |||||
 DB 161 VSY-QTRKNIL-SAIKSPCHRETPPEAEKPM-----YEPYLGAVFQLEKGRLSAE 211
 OY 270 VSNPSILD-PPQDATYFG 286
 |||||

Tue Jul 9 13:21:01 2002

us-09-865-363-11.rpr

Page 8

Db 212 INLPDYLDVAESGQVFG 229

Search completed: July 8, 2002, 20:02:22
Job time: 4231 sec

GA Gallier L.:
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RL and dendritic-cell function".
RL Nature 390:175-179(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Ikeda T.:
CC Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NATIVE T-CELL
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential)..
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC NOT IN NONHEMPOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC TRABECULAR BONE AND LUNG.
CC -I- DISEASE: DEFICIENCY IN TNFSF1 RESULTS IN FAILURE TO FORM LOBULO-
CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC OF NEONBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH
CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDROPLASIA,
CC WITH THICK, IRRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC HYPERTROPHIC CHONDROCYTES.
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; AF053713; AAC40113.1; -;
DR EMBL; AF013170; AAC71061.1; -;
DR EMBL; AB008426; BAA25425.1; -;
DR EMBL; AF019048; AAB6812.1; -;
DR EMBL; AB036798; BAA97259.1; -;
DR MGD; MG1:1100089; Tnfstf1l.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PDO08600; TNF_5; 1.
DR SMART; SMO0207; TNF_1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS0049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KM Signal-anchor. 1
FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT TRANSMEM 49 69 (POTENTIAL).
FT DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CONFLICT 99 99 G -> D (TN REF. 4).
SQ SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

| | | | | |
|-----------------------|--------------|---------------------|---------------|-------------|
| Query Match | 99.6%; | Score 1554; | DB 1; | Length 316; |
| Best Local Similarity | 99.7%; | Pred. No. 3.9e-127; | | |
| Matches 293; | Conservative | 0; | Mismatches 1; | Indels 0; |
| | | | Gaps | 0 |

| | | | |
|----|----|---|-----|
| QY | 1 | GVRHGGRLHNPASVAPAPPPAASRSM LALLLSASQVVSISLDELKNGHNPINAKLQ | 82 |
| DQ | 23 | GVRHGGRLHNPASVAPAPPPAASRSM LALLLSGLQVVSISLFLFYFRAQMPNNISE | 82 |
| QY | 61 | DSTHCFYLLTLHNNADLDOSTLESEDTLPDSCRKMAQAFGANOKELQHLVGPQRSGA | 120 |
| DQ | 83 | DSTHCFYLLTLHNNAGLDOSTLESEDTLPDSCRKMAQAFGANOKELQHLVGPQRSGA | 144 |

QY 121 PAMMEGSLDVAQKGRPEAOEFALLTINAASIPGSHKVLSSMYHDHGAKNISMTLSN 180
Db 143 PAMMEGSLDVAQKGRPEAOEFALLTINAASIPGSHKVLSSMYHDHGAKNISMTLSN 202
QY 181 GKLARNQDGFYYLVANICFRHHETSGSVPEYDYLDMYVYKTSIKIPSSHNLMKGGSTKN 240
Db 203 GKLARNQDGFYYLVANICFRHHETSGSVPEYDYLDMYVYKTSIKIPSSHNLMKGGSTKN 262
QY 241 MSGNEEFHYSINVGGEFKLRAGEEISIQVSNPSLDDPDQATYFGAFKYODID 294
Db 263 MSGNEEFHYSINVGGEFKLRAGEEISIQVSNPSLDDPDQATYFGAFKYODID 316

| | |
|------------|------------|
| RESULT | 2 |
| TN11_HUMAN | |
| ID | TN11_HUMAN |
| STANDARD; | |
| PRT; | 317 AA. |

AC 014788; 014723; Q9P203;
 DT 16-OCR-2001 (Rel. 40, Created)
 DT 16-OCR-2001 (Rel. 40, Last sequence update)
 DT 16-OCR-2001 (Rel. 40, Last annotation update)
 DT 16-OCR-2001 (Rel. 40, Last sequence update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPG) (Osteoclast
 DE differentiation factor) (ODF)
 GN TNFSF11 OR RANKL OR TRANCE OR OPG.

05 Homo sapiens (Human).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
0X NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow, and Peripheral blood;
 RX MEDLINE=98032977; Pubmed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galbert L.;
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).

RN SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=98227661; PubMed=9568710;
 RA Lacey D.L., Trimmis E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarsol I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyte W.J.;
 RT "Osteopontin ligand is a cytokine that regulates osteoclast
 differentiation and activation.";
 RL Cell 93:165-176(1998).

RN [3]
 RN SEQUENCE OF 73-317 FROM N.A.
 RC TISSUE=Thymocytes; Pubmed=9312132;
 RX MEDLINE=97460112;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlicknick J., Chao M.,
 RA Kalschthal S., Cayani E., Battlert F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "GRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells";
 RL J. Biol. Chem. 272:25190-25194(1997).

| | |
|----|---------------------------------|
| RN | [4] |
| RP | SEQUENCE FROM N.A. (ISOFORM 2) |
| RC | TISSUE=Tongue; |
| RX | MEDLINE=20175237; Pubmed=107081 |

RA Nagai M., Kyakumoto S., Sato N.:
RT "Cancer cells responsible for humoral hypercalcemia express mRNA
RT encoding a secreted form of ODF/TRANCE that induces osteoclast
RT formation.";
RL Biochem. Biophys. Res. Commun. 269:532-536 (2000).

CC -I- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELLS
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC

CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
CC AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
CC HYPERCALCAEMIA OF MALIGNANCY.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
CC SECRETED (ISOFORM 2).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: AF019047; AAB86811.1; -
DR EMBL: AF053712; AAC39731.1; -
DR EMBL: AF013171; AAC51762.1; -
DR EMBL: AB037599; BAA90488.1; -
DR MIM: 602642; -
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; FALSE_NEG.
DR PROSITE: PS00049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor; Alternative splicing
FT DOMAIN 1 47 CYTOSOLSMIC (POTENTIAL).
FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 69 317 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1 73 MISSING (IN ISOFORM 2).
FT CONFLICT 194 194 A -> G (IN REF. 3).
SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;

Query Match 85.0%; Score 1326.5; DB 1; Length 317;
Best Local Similarity 84.5%; Pred. No. 1.8e-107;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

OY 1 GVPHEGLHPAPAPAPAPAPAPASRSMFLALLGLGLGVVCSIALFLYFRAQNDPRRISE 60
DB 23 GAPHEGLH-APPPAPHPAPAPASRSMFLALLGLGLGVVCSIALFLYFRAQNDPRRISE 81
OY 61 DSTHCFRILRLHNLALDOSTLESEPT--LPDSCRMKAQFGAVOKELQHTVGPQRS 118
DB 82 DCHCTFRILRLHNLALDOSTLESEPT--LPDSCRMKAQFGAVOKELQHTVGPQRS 141
OY 119 GAPAMMGSLVDVQGRKPEAPFAHLITNASTIPSGSHKVTLSWHDGNAKISMTL 178
DB 142 AEKAMVGSMLDLAKRKLKLEQPPAHLITNATIPSGSHKVTLSWHDGNAKISMTL 201
OY 179 SNGKLAVNODGFYLLVANICFRHHTSGSVPTDYLQMLVTVVTSIKIPSSHMLMGSGST 238
DB 202 SNGKLAVNODGFYLLVANICFRHHTSGDLATEYLQMLVTVVTSIKIPSSHMLMGSGST 261
OY 239 KNSGNSSEPHFYSINNGGFEKRLAGEEISIQVSPSLDDPDQATITYGAKVQDID 294
DB 262 KYMSGNSEPHFYSINNGGFEKRLAGEEISIEVSNPSLLDDPDQATITYGAKVQDID 317

RESULT 3

TN10_HUMAN
ID TN10_HUMAN STANDARD: PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
GN apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
OS TNFSL10 OR TRAIL OR Apo2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis.";
RL Immunity 3:673-682(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96278649; PubMed=8663110;
RA Pitti R.M., Masters S.A., Ruppert S., Donahue C.J., Moore A.,
RA Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family.";
RL J. Biol. Chem. 271:12687-12690(1996).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX MEDLINE=20017054; PubMed=10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullrich M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed=10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Srean G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).
CC -1- FUNCTION: INDUCES APOPTOSIS.
CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
CC AND PROSTATE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: U37518; AAC50332.1; -
DR EMBL: U57059; AAB01233.1; -
DR MIM: 603598; -
DR PDB: 1D0G; 22-OCT-99.
DR PDB: 1D4V; 01-NOV-99.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.


```

Db      216 PGDLVLMTE-EKRLNCTCTGQIWAHSHSYLGLAVFNLTVDHDLVYNLSQSLINFESENFTFG 274
OY      287 AFKV 290
       :|:
Db      275 LYKL 278

RESULT      7
FASL_MOUSE STANDARD: PRT: 279 AA.
AC PA1047; Q61217; Q9RIE2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FAS antigen ligand.
GN TNFSE OR APTLIG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
[1]
RN RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX RX MEDLINE=94185175; PubMed=7511063;
RA RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL RL Cell 76:969-976(1994).
[2]
RN RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RP RP STRAIN-C57BL/6;
RC RC MEDLINE=95388076; PubMed=7544870;
RX RX Peltsch M.J., Tschopp J.J.;
RA RA "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL RL Mol. Immunol. 32:761-772(1995).
[3]
RN RP SEQUENCE FROM N.A. (ISOFORM FASL).
RP RP MEDLINE=95196085; PubMed=7894405;
RX RX Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT RT "Type mouse fas-ligand gene is mutated in gld mice and is part of a
RL TNF family gene cluster.";
RN RN Immunity 1:131-136(1994).
[4]
RN RP SEQUENCE FROM N.A. (ISOFORM FASL).
RP RP STRAIN-BALB/C;
RC RC Fener M.H., Shioda T., Isselbacher K.J.;
RA RA "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids.";
RL RL Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
[5]
RN RP SEQUENCE FROM N.A. (ISOFORM FASL).
RP RP STRAIN-C3H; TISSUE=Spleen;
RC RC MEDLINE=20021694; PubMed=10552956;
RA RA Ayrolat E., D'Adamio F., Zollo O., Agostini M., Morra R.,
RA Camarille L., Migliorati G., Delfino D.V., Riccardi C.;
RT RT "Cloning and expression of a short Fas ligand: A new alternatively
RL spliced product of the mouse Fas ligand gene.";
RN RN Blood 94:3456-3467(1999).
[6]
RN RP CHARACTERIZATION OF VARIANT GLD.
RX RX MEDLINE=96091792; PubMed=7495745;
RA RA Haime M., Peltsch M.C., Immler M., Schroeter M., Lowin B.,
RT Roussseau M., Bion C., Rensu T., French L., Tschopp J.;
RL RL "Characterization of the non-functional Fas ligand of gld mice.";
CC CC Int. Immunol. 7:1381-1386(1995).
-1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE

```

| Query Match | Best Local Similarity | Score 177; | DB 1; | Length 279; |
|--|------------------------------------|----------------|------------|-------------|
| Matches 70; | Conservative 46; | Mismatches 97; | Indels 92; | Gaps 13 |
| QY 3 PHEGPLHPADAPADP | -----PAASRSKFTLLDLGLGQVVCSTALFL 47 | 11.3%; | DB 1; | Length 279; |
| DB 50 PPSQPLPPSSQPLPLPLPLPLKPKKDHNTLMPLVVFVMTVALVGMGLG-----MKQ 101 | -----PAPSRSKFTLLDLGLGQVVCSTALFL 47 | 11.3%; | DB 1; | Length 279; |
| QY 48 YEKADMDPNRISDTHCFRILRLHENADLDOSTIESEDTLPDSCRMKQAFQAVOKE 107 | -----LREFNDSLKSTSEKQIANST----- 134 | 11.3%; | DB 1; | Length 279; |
| DB 102 LFHLQKE--LAE-----LREFNDSLKSTSEKQIANST----- 134 | -----LREFNDSLKSTSEKQIANST----- 134 | 11.3%; | DB 1; | Length 279; |
| QY 108 LQHVGFQFQSGAPAMMEGSLMDVAORGKREAPFAHLITN--AASIPSGSHKVTLLSSWY 165 | -----LREFNDSLKSTSEKQIANST----- 134 | 11.3%; | DB 1; | Length 279; |
| DB 135 -----PSE-----KPEPSVAHLITNPHSRISIP-----LEWE 161 | -----LREFNDSLKSTSEKQIANST----- 134 | 11.3%; | DB 1; | Length 279; |

QY 166 HDGMAKISMTLSNCKLRVNDGFFYYLVANICFRHHTSGSVPTDYLQMLVYVYKTSIK 225
DB 162 DTYGATLISCVKRYKGGVLTNETGLTFVYKSKYFR--GSCNNPLNH---KYVM--RNSK 215
QY 226 IPSSHNLKMGKSTKMSGSEFFHYSLNVCGEFKLRAGEISIOVSNPSLLDPDQATF 285
DB 216 YPDDVLVME-EKRLNVCCTTGQTMAHSSYLGAVNLTSAHLVYVNSLTLNFEESKTF 274
QY 286 GAFKV 290
DB 275 GLYKL 279

RESULT 8
FAST_HUMAN STANDARD: PRT: 281 AA.
ID P48023;
DT 01-FEB-1996 (rel. 33, Created)
DT 01-FEB-1996 (rel. 33, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE FAS antigen ligand (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN TNFSF6 OR APTL1G1 OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T lymphocytes".
RL J Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species specificity".
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Schetelig C.E., Poehmann R., Philippen P., Elbel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RX Fushimoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus infection".
RL Blochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP TISSUE=Blood.
RC Matsunuma M., Nakanishi Y., Ohba Y.;
RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT. FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL SURFACE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD178 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/3338769674.g.htm".
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CC -----
DB EMBL; X89102; CAA61474.1; -
DB EMBL; U08137; AAC50071.1; -
DB EMBL; U11821; AAC50124.1; -
DB EMBL; D38122; BAA07320.1; -
DB EMBL; 296050; CAB09424.1; -
DB EMBL; AB013303; BAA32542.1; -
DB HSP; P06804; TNF.
DB MIM; 134638; -
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_ab.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_ab; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1.
DR SMART; SM00251; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;
FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 70 PRO-RICH.
FT DOMAIN 45 65 POLY-PRO.
FT DISULFID 202 233 BY SIMILARITY.
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 281 AA; 31485 MW; ABA6EB358246E9BB CRC64;
Query Match 11.18; Score 174; DB 1; Length 281;
Best Local Similarity 21.88; Pred. No. 7.4e-08;
Matches 67; Conservative 43; Mismatches 104; Indels 94; Gaps 10;
QY 3 PHEGPLHAPSPAPAP-----PPAASRS-----MFLALGLGIGVGVCSIA 44
DB 48 PPPPPPLPPPPPPPLPLPLPLKRGKNSSTGLCLVFFMVLVALVGLG----- 100
QY 45 LELYFRAQMDPNRISSEDSTNCFYRIILRLHENDLQDSTLESDTLDPSCRMRKQAFQAV 104
DB 101 MFOLFHLQ-----KELALRESTSGMHTA-----SSL 127
QY 105 OKELQHVGPQRFSGAPAMMEGSLDYAQRKPEAPFAFLT--INAASTPSCSHVVTLS 162
DB 128 EKQIGHSPPE-----KKELRVALLTKSNSRSRP-----L 160
QY 163 SWYHRCMAKISMTLSNCKLRVNDGFFYYLVANICFRHHTSGSVPTDYLQMLVYVYKTSIK 225
DB 161 EWEDYGVIVLSCVKKYKGGVLTNETGLTFVYKSKYFR--GSCNNPLNH---LPLSHVYK 214
QY 223 STIPSSHNLKMGKSTKMSGSEFFHYSLNVCGEFKLRAGEISIOVSNPSLLDPDQATF 285
DB 215 NSRYPDVLVME-GKMMSYCTTGQMAHSSYLGAVNLTSAHLVYVNSLTLNFEESKTF 274
QY 283 TYFGAFKV 290
DB 274 TFGGLYKL 281

RESULT 9
TNFS_HUMAN STANDARD: PRT: 261 AA.
ID TNFS_HUMAN

AC P29965;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCR-2001 (Rel. 40, Last annotation update)
 DE CD40 ligand (CD40-L) (TNF-related activation protein) (TRAP) (T cell
 DE antigen gp39) (CD134 antigen).
 GN TNFSF5 OR CD40LG OR CD40L OR TRAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93076854; PubMed=1280226;
 RA Graf D., Korthauer U., Mages H.W., Senger G., Kroccek R.A.;
 RT "Cloning of TRAP, a ligand for CD40 on human T cells.";
 RL Eur. J. Immunol. 22:3191-3194(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93049181; PubMed=1385114;
 RA Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,
 RA Briesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,
 RA Aruffo A.;
 RT "The human T cell antigen gp39, a member of the TNF gene family, is a
 RT ligand for the CD40 receptor: expression of a soluble form of gp39
 RT with B cell co-stimulatory activity.";
 RL EMBO J. 11:4313-4321(1992).
 RN [3]
 RP SEQUENCE FROM N.A. AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.
 RX MEDLINE=93145530; PubMed=7678782;
 RA Aruffo A., Farrington M., Hollenbaugh D., Li X., Mlatovich A.,
 RA Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M.,
 RA Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;
 RT "The CD40 ligand, gp39, is defective in activated T cells from
 RT patients with X-linked hyper-IgM syndrome.";
 RL Cell 72:291-300(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93094757; PubMed=1281209;
 RA Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,
 RA Macculif B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
 RT "Recombinant human CD40 ligand stimulates B cell proliferation and
 RT immunoglobulin E secretion.";
 RL J. Exp. Med. 176:1543-1550(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93138085; PubMed=7678552;
 RA Gauchat J.F.M., Aubry J., Mazzei G.J., Ilfe P., Jomotte T., Elson G.,
 RA Bonnefoy J.Y.;
 RT "Human CD40-ligand: molecular cloning, cellular distribution and
 RT regulation of expression by factors controlling IgE production.";
 RL FEBS Lett. 313:259-266(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,
 RA Matsuda I.;
 RT Submitted (FEB-1995) to the EMBL/GenBank/DBS databases.
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
 RX MEDLINE=96131874; PubMed=8589998;
 RA Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
 RA Chess L., Thomas D.;
 RT "2-A crystal structure of an extracellular fragment of human CD40
 RT ligand.";
 RL Structure 3:1031-1039(1995).
 RN [8]
 RP 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.
 RX MEDLINE=9826353; PubMed=9605317;
 RA Sinoh J., Garber E., Van Viljmen H., Karpusas M., Hsu Y.-M.,
 RA Zheng Z., Naismith J.H., Thomas D.;
 RT "The role of polar interactions in the molecular recognition of CD40L
 RT with its receptor CD40.";
 RL Protein Sci. 7:1124-1135(1998).

RN [9]
 RP VARIANTS HIGM1 ARG-36 AND GLY-140.
 RX MEDLINE=93156839; PubMed=7679206;
 RA Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,
 RA Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,
 RA Kroccek R.A.;
 RT "Defective expression of T-cell CD40 ligand causes X-linked
 RT immunodeficiency with hyper-IgM.";
 RL Nature 361:539-541(1993).
 RN [10]
 RP VARIANT HIGM1 GLU-123.
 RX MEDLINE=93156840; PubMed=8094231;
 RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,
 RA de Saint Basile G.;
 RT "CD40 ligand mutations in X-linked immunodeficiency with hyper-IgM.";
 RL Nature 361:541-543(1993).
 RN [11]
 RP VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227.
 RX MEDLINE=93174270; PubMed=7679801;
 RA Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,
 RA Copeland N.G., Bedell M.A., Edelhoff S., Distèche C.M.,
 RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;
 RT "CD40 ligand gene defects responsible for X-linked hyper-IgM
 RT syndrome.";
 RL Science 259:990-993(1993).
 RN [12]
 RP VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
 RX MEDLINE=9523438; PubMed=7717401;
 RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnoli D.,
 RA Gillani S., Mantuano E., Fasch A., Andersson B., Zegers B.J.M.,
 RA Cavaiani G., Reznick I., Levy J., Zan-Bar I., Porat Y., Alro P.,
 RA Plebani A., Vezzoni P., Notarangelo L.D.;
 RT "Characterization of nine novel mutations in the CD40 ligand gene in
 RT patients with X-linked hyper IgM syndrome of various ancestry.";
 RL Am. J. Hum. Genet. 56:898-906(1995).
 RN [13]
 RP VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219.
 RX MEDLINE=96133533; PubMed=8550833;
 RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,
 RA Gatti R.A., Deruef D.C., Belmont J.W., Conley M.E.;
 RT "A single strand conformation polymorphism study of CD40 ligand.
 RT Efficient mutation analysis and carrier detection for X-linked hyper
 RT IgM syndrome.";
 RL J. Clin. Invest. 97:196-201(1996).
 RN [14]
 RP VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.
 RX MEDLINE=97295077; PubMed=9150729;
 RA Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer M.,
 RA Yata J.-I., Ochs H.D.;
 RT "Mutations of the CD40 ligand gene in 13 Japanese patients with
 RT X-linked hyper-IgM syndrome.";
 RL Hum. Genet. 99:624-627(1997).
 CC -I- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
 CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
 CC -I- SUBUNIT: HOMOTRIMER.
 CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM.
 CC -I- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
 CC T-LYMPHOCYTES.
 CC -I- DISEASE: DEFECTS IN TNFSF5 ARE THE CAUSE OF AN X-LINKED
 CC IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1). AN IMMUNOGLOBULIN ISOTYPE
 CC SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM
 CC IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES
 CC PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)
 CC RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
 CC PNEUMOCYSTIS CARINITI PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
 CC CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
 CC INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
 CC WITH A DEATH RATE OF ABOUT 10% BEFORE ADULESCENCE.
 CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -I- DATABASE: NAMB=CD40base;
 CC NOTE=European CD40L defect database (mutation db);


```

CC WWW="http://www.expasy.org/cdd401base/";
CC FTP="ftp://ftp.expasy.org/databases/cdd401base";
CC -1 DATABASE: NAME=PROV; NOTE=CD guide CD154 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/proc/cdd401base.htm"
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CC -----
DR EMBL; X68550; CAA8554.1; -
DR EMBL; Z15017; CAA7873.1; -
DR EMBL; X67878; CAA4807.1; -
DR EMBL; L07414; AAA35662.1; -
DR EMBL; D31797; BAA06599.1; -
DR EMBL; D31793; BAA06599.1; JOINED.
DR EMBL; D31794; BAA06599.1; JOINED.
DR EMBL; D31795; BAA06599.1; JOINED.
DR EMBL; D31796; BAA06599.1; JOINED.
DR PIR; S26684; S26684.
DR PIR; S26694; S26694.
DR PIR; S28017; S28017.
DR PIR; S28852; S28852.
DR PIR; JH0793; JH0793.
DR PDB; 1ALY; 17-SEP-97.
DR MIM; 308230; -
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytochrome; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
KW Domain; Disease mutation; Polymorphism.
FT DOMAIN 1 22 CYTOPLASMIC.
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 47 261 EXTRACELLULAR (POTENTIAL).
FT DISULFID 178 218 POTENTIAL.
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 36 36 M -> R (IN HIGM1).
FT VARIANT 123 123 A -> E (IN HIGM1).
FT VARIANT 126 126 V -> A (IN HIGM1).
FT VARIANT 128 129 /FTID-VAR_007515.
FT VARIANT 140 140 SE -> RG (IN HIGM1).
FT W -> C (IN HIGM1).
Query Match 10.9%; Score 169.5; DB 1; Length 261;
Best Local Similarity 25.7%; Pred. No. 1.6e-07;
Matches 75; Conservative 50; Mismatches 116; Indels 51; Gaps 16;

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OY 239 KMWGNGSEPHRSTINVGGEFKAGEEISTQVNSPLDDQATYRGARKV 290
DB 212 H--SSAKPCGGQSTHLDGVEFELPGASVFNWYDPSVSHGTGFTSLGLKL 261
RESULT 10
TNF5_FELCA STANDARD; PRT; 260 AA.
AC 097605;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD40 ligand (CD154 antigen).
GN TNFSP5 OR CD40LG OR CD40L.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Hosie M.J., Willett B.J.;
RT Adjuvant properties of feline CD154 (CD40 ligand).";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF079105; AAD02954.1; -
DR HSSP; P29965; 1ALY.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytochrome; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 47 260 EXTRACELLULAR (POTENTIAL).
FT DISULFID 177 217 POTENTIAL.
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 260 AA; 28727 MW; 349FA0391FB7B32 CRC64;
Query Match 10.7%; Score 167; DB 1; Length 260;
Best Local Similarity 25.4%; Pred. No. 2.7e-07;
Matches 74; Conservative 50; Mismatches 117; Indels 50; Gaps 16;

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DR 111 -----AMOGQDPRVAHV-ISRAS-----SSTASVLQW-APKGYITSSMLVLENNKQ 159
DB 183 LRVNODGEFYLYANICF-RHHETSGSVPTDYLOLMVYVKTISIKIPSSH-N-LMKGGSTK 239
QY 160 LAVKROGLYIYAQVTFCSNRASQAP-----FIASLCHSPSGSERVLLRAANAR 211
DB 240 NMSGNSEHFHSINVGFEFKLRAGEISIOVNSPSLDDPPDADATYFGAFKY 230
DB 212 -SSSKPCGQGSIHGQGYELHPGASVFNVTDPQSQVSHGTSTFGLKL 260

RESULT 11
TNFA.CANFO STANDARD: PRT: 234 AA.
AC PS1435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (cachectin).
GN TNF OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE-Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-DUNKIN-HARTLEY;
RA MEDLINE-97462215; PubMed-9316485;
RA White A.W., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U39839; AAB06492.1; -
DR EMBL: U77036; AAB19210.1; -
DR HSSP: P06804; 2TNF.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNCRSISICT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.

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DR PROSITE: PS0049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 79 BY SIMILARITY.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 147 178 BY SIMILARITY.
SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 10.1%; Score 157; DB 1; Length 234;
Best Local Similarity 26.1%; Pred. No. 1.7e-06;
Matches 54; Conservative 26; Mismatches 65; Indels 62; Gaps 9;

QY 111 IVGPOR---FSGAPAMMGSWLDVAORKEPEAQ-----PFAHLITNAAIP 153
DB 55 VIGPQREQSSGPPF-----RPLAQTLIRASQNDNDKPVAVHANQQAEE 102
QY 154 SGSHKVTLSWYHGRGAKISN-WTLSNGKLVRNODGEFYLYANICFRHHETSGSVPTDY 212
DB 103 E-----LQWLSKRAVALLANGMGLSDNQLVPSDGLYLIVSQVLPK-----GQGCPSY 150
QY 213 LQIMVYVKTISIKIPSSINLM-----KGGSTKNMSGSEHFHSINVGFEFKL 260
DB 151 LLHTHTVSRLAVSYPEKYNLISAIKSPQKETPGAEKRW-----YEPYILGVGFOL 203
QY 261 RAGEISIOVNSPSLDD-PPDADATYFG 286
DB 204 QKGDRLSAEVLNLPYLDPFADSGQIYFG 230

RESULT 12
TNFS.CANFA STANDARD: PRT: 260 AA.
AC 097626;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD40 ligand.
GN TNFSF5 OR CD40LG OR CD40L.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Hosie M.H., Willett B.J.;
RT "Adjuvant properties of canine CD40L.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF086711; AAD04375.1; -
DR HSSP: P29965; 1ALY.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRODOM: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.

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KM Cytokine: Transmembrane; Glycoprotein; Signal-anchor.
 FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 47 260 (POTENTIAL).
 FT DISULFID 177 217 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 239 239 POTENTIAL.
 SQ SEQUENCE 260 AA: 28688 MW: 6046919e98EB70 CRC64;

Query Match 10.1%; Score 157; DB 1; Length 260;
 Best Local Similarity 25.5%; Pred. No. 2e-06;
 Matches 75; Conservative 50; Mismatches 113; Indels 56; Gaps 17;

OY 11 APSADAPAPPPAASRSMFLALIGLGLGVVCSIALF-LYFRAOM----DPNRISDSTHIC 65
 DB 9 APRSAVATGPP-VSMKIFMYLTLVFLITQMGSALEFAYVLRRLDKIDENIYED--FV 64
 OY 66 FYRIIRLHFNADLDOSTLESDTLPDSRRMKOAFQGVOKELOHIVGPQRFSGAPAME 125
 DB 65 FPKTLQKCNKGGSLSL-----NCEIKSQPE-AFLKEIM-LNNEMKEENIAM-- 112
 OY 126 GSWLDVAORGRPEAOPFAHLITINASIPSGSHKVTLSWYHIDRGMAKISN--MTLSNGK- 182
 DB 113 -----QKGDOPRIAAHVISEASNP-----SVLRW-APKGYTTISMLVSELENGKQ 159
 OY 183 LRVNODGFYLYLANICF-RHHETSGSVPTDYQLVMVYVVKTSIKIPSSH--LKKGGSTK 239
 DB 160 LAVKHQGLYVYAQVTFCSNRAASQAP-----FVASLCLHSPSTENVLLRAASSR 211
 OY 240 MMS---GMSERHFYSINCGFPKLRAGEIIOVSNPSLDDPPDDATYFGAFKV 290
 DB 212 GSKKPCGGQ-----SHLGVEFLHPCASVFNVTDPDSQVSHGTGTFSGFLKL 260

RESULT 13
 TNFS_MOUSE STANDARD; PRT; 260 AA.
 AC P27548: 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen GP39)
 DE TNFS5 OR CD40LG OR CD40L.
 CN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92244364; PubMed=1374165;
 RA Armitage R., Fanslow W., Sato T.A., Clifford K.N., Strockbine L., Macduff B.M., Anderson D.M., Gimpel S.D., Davis-Smith T., Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D., Springer M.K.;
 RT "Molecular and biological characterization of a murine ligand for CD40.";
 RT Nature 357:80-82(1992).
 RL Nature 357:80-82(1992).
 RN [2]
 RP REVISION TO 199.
 RA Spriggs M.K.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SIMILARITY TO THE TNF FAMILY.
 RX MEDLINE=92310561; PubMed=1377364;
 RA Farrah T., Smith C.A.;
 RT "Emerging cytokine family.";
 RL Nature 358:26-26(1992).
 RN [4]
 RP 3D-STRUCTURE MODELING OF 115-260.
 RX MEDLINE=93200072; PubMed=8095800;
 RA Peitsch M.C., Jongeneel C.V.;

RT "A 3-D model for the CD40 ligand predicts that it is a compact trimer similar to the tumor necrosis factors.";
 RT Int. Immunol. 5:233-238(1993).
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+ T-LYMPHOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC EMBL: X65453; CAA46448.2; ..
 CC DR PIR; S21738; S21738.
 CC DR PDB; ICDA; 31-OCT-93.
 CC DR MGD; MGI:88337; Tnf5f5.
 CC DR InterPro; IPR003263; Tnf5f5.
 CC DR InterPro; IPR000478; Tnf_family.
 CC DR Pfam; PF00229; Tnf_1.
 CC DR ProDom; PD008600; Tnf_5; 1.
 CC DR SMART; SM00207; Tnf_1.
 CC DR PROSITE; PS00251; Tnf_1; 1.
 CC DR PROSITE; PS00449; Tnf_2; 1.
 CC CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure.
 FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 46 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 47 260 (POTENTIAL).
 FT DISULFID 177 217 POTENTIAL.
 FT CARBOHYD 239 239 N-LINKED (GLCNC. . .) (POTENTIAL).
 SQ SEQUENCE 260 AA: 29370 MW: 7E1AC117473672AD CRC64;

Query Match 9.8%; Score 153; DB 1; Length 260;
 Best Local Similarity 24.9%; Pred. No. 4.4e-06;
 Matches 74; Conservative 53; Mismatches 110; Indels 60; Gaps 16;

OY 10 PASAARAPPPAASRSMFLALIGLGLGVVCSIALF-LYFRAOMDPNRISDSTHICFYR 68
 DB 8 PSPRSVATGLP-ASMKIFMYLTLVFLITQMGSALEFAYVLRRLD--KVEEE----- 56
 OY 69 ILRLHEN-----ADLDOSTLESDTLPDSRRMKOAFQGVOKELOHIVGPQRFSG 119
 DB 57 -VNLHDEPFYIKLKCNKGGSLSLNCEENKROFEDLVKDTLNKE----- 103
 OY 120 APAMGMSWLDVAORGRPEAOPFAHLITINASIPSGSHKVTLSWYHIDRGMAKISNM-T 178
 DB 104 --EKRENSF--EMORGDDEDPQIAAHVSEA-----NSNAAVLQNAKKGYITMKSNLVL 154
 OY 179 SNGK-LRVNODGFYLYLANICF-RHHETSGSVPTDYQLVMVYVVKTSIKIPSSH--LM 233
 DB 155 ENKQLTVRREGLYVYVTVTFCSSNRPSSORP-----FIVGLWLK-PSSGSERLIL 205
 OY 234 KGSSTKMGSGNSEHFYSINCGFPKLRAGEIIOVSNPSLDDPPDDATYFGAFKV 290
 DB 206 KAANTHSSQLOEQO--SVHLGVEFLQMGASVFNVTASOIVHRVGFSSGLLKL 260

RESULT 14
 TNFA_HORSE STANDARD; PRT; 234 AA.
 AC P29553: 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
 GN TNF OR TNFA.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NC NCBL_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92084125; PubMed=1748301;
 RA Su X., Morris D.D., McGraw R.A.;
 RT "Cloning and characterization of gene TNF alpha encoding equine tumor
 necrosis factor alpha.";
 RL Gene 107:319-321(1991).
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M64087; AAA30959.1; -
 DR PIR: J01344; J01344.
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
 KW PROPEP 1 77 BY SIMILARITY.
 FT CHAIN 78 234 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 146 178 BY SIMILARITY.
 FT SEQUENCE 234 AA; 25469 MW; E79AC91143DE373 CRC64;
 SQ
 Query Match 9.5%; Score 149; DB 1; Length 234;
 Best Local Similarity 24.1%; Pred. No. 8.5e-06;
 Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

DB 216 PNLYDEAESGQVYFG 230
 RESULT 15
 ID TNFA_MACEFA STANDARD; PRT; 233 AA.
 AC P79337;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
 GN TNF OR TNFA.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 NC Cercopithecoidea; Macaca.
 NC NCBL_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Lymphocytes;
 RA Tatum M.;
 RT Submitted (JAN-1997) to the EMBL/Genbank/DDJ databases.
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB000513; BAA19131.1; -
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
 KW PROPEP 1 76 BY SIMILARITY.
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 145 177 BY SIMILARITY.
 FT SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;
 SQ
 Query Match 9.5%; Score 148.5; DB 1; Length 233;
 Best Local Similarity 25.6%; Pred. No. 9.3e-06;
 Matches 50; Conservative 38; Mismatches 68; Indels 39; Gaps 11;

Qy 166 HDGMAKISN-WTLSNGKLRVNODGFYLYANICERHHETSGSVPTDYQL-----M 216
Db 106 NRRANALVANGVELTDNQLVPSSEGLYLYISOVLEK---GOGCPSNHVLTHTTISR IAY 161
Qy 217 VYVVK---TSIKIPSSHNLKMGSGTKMNSGSEPHFYISINVGCFPKLRAGEEISIQVSN 272
Db 162 SYOTKYNLSSAIKSPCQRETPPGAEAKPW-----YEPYILGIVGFQLEKGDRLSAEINTL 214
Qy 273 PSLLD-PQODATYFG 286
Db 215 PDYLDFAESGQVYFG 229

Search completed: July 8, 2002, 18:51:49
Job time: 17487 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 16:22:56 ; Search time 119.9 Seconds
(without alignments)
424.191 Million cell updates/sec

Title: US-09-865-363-11

Perfect score: 1561
Sequence: 1 GVPHECPRLHPAPSAPAPAP.....LDDPDQDATYFGAFKQDID 294

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_ORNITHINE:*
8: SP_ORNITHINE:*
9: SP_ORNITHINE:*
10: SP_PLANT:*
11: SP_PROTIST:*
12: SP_VIRUS:*
13: SP_VIRUS:*
14: SP_VIRUS:*
15: SP_VIRUS:*
16: SP_VIRUS:*
17: SP_VIRUS:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------------|
| 1 | 1525.5 | 97.7 | 313 | 11 | Q9RIY0 mus musculus |
| 2 | 1492 | 95.6 | 318 | 11 | Q9SESE2 rat mus musculus |
| 3 | 1426 | 91.4 | 287 | 11 | Q9JJK9 mus musculus |
| 4 | 1227 | 78.6 | 270 | 4 | Q96Q17 mus musculus |
| 5 | 1057 | 67.7 | 199 | 11 | Q9JJK8 mus musculus |
| 6 | 272 | 17.4 | 53 | 11 | Q9JJK8 mus musculus |
| 7 | 263.5 | 16.9 | 214 | 13 | Q9JJK8 mus musculus |
| 8 | 218.5 | 14.0 | 287 | 13 | Q9JJK8 mus musculus |
| 9 | 186.5 | 11.6 | 261 | 6 | Q9JJK8 mus musculus |
| 10 | 180.5 | 11.5 | 261 | 6 | Q9JJK8 mus musculus |
| 11 | 179 | 11.5 | 280 | 6 | Q9JJK8 mus musculus |
| 12 | 177 | 11.3 | 280 | 6 | Q9JJK8 mus musculus |
| 13 | 175 | 11.2 | 280 | 6 | Q9JJK8 mus musculus |
| 14 | 174.5 | 11.2 | 261 | 6 | Q9JJK8 mus musculus |
| 15 | 173 | 11.1 | 282 | 6 | Q9JJK8 mus musculus |
| 16 | 172.5 | 11.1 | 272 | 13 | Q9JJK8 mus musculus |

| | | | | | | |
|----|-------|------|-----|----|---------|-------------------------|
| 17 | 172.5 | 11.1 | 282 | 6 | Q9BEA8 | Q9BEA8 sus scrofa |
| 18 | 172.5 | 11.1 | 282 | 6 | Q9SM04 | Q9SM04 sus scrofa |
| 19 | 152 | 9.7 | 240 | 6 | Q9BDM7 | Q9BDM7 macaca nemo |
| 20 | 149 | 9.5 | 234 | 6 | Q9TJ3 | Q9TJ3 equus caball |
| 21 | 148 | 9.5 | 232 | 11 | Q9SM83 | Q9SM83 mus musculus |
| 22 | 147.5 | 9.4 | 310 | 11 | Q9JMK10 | Q9JMK10 macaca nemo |
| 23 | 143 | 9.2 | 260 | 11 | Q9Z2V2 | Q9Z2V2 rat mus musculus |
| 24 | 143 | 9.2 | 260 | 11 | Q9Z2V2 | Q9Z2V2 rat mus musculus |
| 25 | 142.5 | 9.1 | 239 | 11 | Q9QYH9 | Q9QYH9 mus musculus |
| 26 | 142 | 9.1 | 232 | 4 | Q9JMK11 | Q9JMK11 macaca nemo |
| 27 | 140.5 | 9.0 | 310 | 11 | Q9JMK11 | Q9JMK11 macaca nemo |
| 28 | 140 | 9.0 | 174 | 4 | Q9S150 | Q9S150 homo sapien |
| 29 | 139 | 8.9 | 234 | 6 | Q9S150 | Q9S150 homo sapien |
| 30 | 136 | 8.7 | 191 | 6 | Q9WY22 | Q9WY22 capra hircu |
| 31 | 133.5 | 8.6 | 215 | 11 | Q9JND1 | Q9JND1 tamiasciuru |
| 32 | 133 | 8.5 | 157 | 4 | Q43647 | Q43647 homo sapien |
| 33 | 132 | 8.5 | 149 | 6 | Q97543 | Q97543 actus nancy |
| 34 | 132 | 8.5 | 217 | 11 | Q9ERG6 | Q9ERG6 peromyscus |
| 35 | 131.5 | 8.4 | 156 | 11 | Q9JMK14 | Q9JMK14 sigmodon hl |
| 36 | 131 | 8.4 | 149 | 6 | Q97538 | Q97538 actus vocif |
| 37 | 131 | 8.4 | 149 | 6 | Q97538 | Q97538 actus vocif |
| 38 | 130 | 8.3 | 204 | 4 | Q9JMK12 | Q9JMK12 homo sapien |
| 39 | 130 | 8.3 | 216 | 11 | Q70332 | Q70332 mesocricetu |
| 40 | 128.5 | 8.2 | 233 | 6 | Q9BEA1 | Q9BEA1 tenrec ecau |
| 41 | 127.5 | 8.2 | 217 | 6 | Q9BEC5 | Q9BEC5 tenrec ecau |
| 42 | 126.5 | 8.1 | 217 | 6 | Q9BEC1 | Q9BEC1 tenrec ecau |
| 43 | 126.5 | 8.1 | 217 | 6 | Q9BEC0 | Q9BEC0 tenrec ecau |
| 44 | 126.5 | 8.1 | 220 | 6 | Q9X747 | Q9X747 macropus eu |
| 45 | 126 | 8.1 | 216 | 6 | Q9BEC9 | Q9BEC9 ochotona pr |

ALIGNMENTS

| RESULT | ID | PRELIMINARY | PRT | 313 AA. |
|----------|--|----------------------------|-----|---------|
| Q9RIY0 | Q9RIY0 | | | |
| AC | Q9RIY0 | | | |
| DT | 01-MAY-2000 (TREMBL) | 13, Created | | |
| DT | 01-MAY-2000 (TREMBL) | 13, Last sequence update | | |
| DT | 01-DEC-2001 (TREMBL) | 19, Last annotation update | | |
| DE | OSTEOCLAST DIFFERENTIATION FACTOR. | | | |
| GN | TNFSF11. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_Taxid=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | SYRAIN=129; | | | |
| RX | MEDLINE=99214075; PubMed=10196481; | | | |
| RA | Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A., | | | |
| RT | Ueda M., Higashio K., | | | |
| RT | "Cloning and characterization of the gene encoding mouse osteoclast | | | |
| RL | differentiation factor." | | | |
| EMBL | Gene 230:121-127(1999). | | | |
| EMBL | AB022036; BAA36970.1; - | | | |
| EMBL | AB022037; BAA36970.1; JOINED. | | | |
| EMBL | AB022038; BAA36970.1; JOINED. | | | |
| HSSP | P50591; ID06. | | | |
| MCD | MGI:1100089; Tnfsf11. | | | |
| InterPro | IPR003263; TNF-5. | | | |
| InterPro | IPR000478; TNF_family. | | | |
| Pfam | PF00229; TNF_1. | | | |
| PRODOM | PD008600; TNF_5; 1. | | | |
| SMART | SM00207; TNF_1. | | | |
| PROSITE | PS50049; TNF_2; 1. | | | |
| SEQUENCE | 313 AA; 34719 MW; 37D530B8BFC2842E CRC64; | | | |

Query Match 97.7%; Score 1525.5; DB 11; Length 313;
Best Local Similarity 98.6%; Pred. No. 1.5e-132;

DE HRANKL2.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RA
RA Ikeda T., Kuroyama H., Hirokawa K.,
RT "Human RANKL Isoform."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB061827; BAB71768.1; --
SQ SEQUENCE 270 AA; 30522 MW; 5C7754CE32BEF368 CRC64;

| | | | | |
|-----------------------|-----------------|---|----------|------------|
| Query Match | 78.6% | Score 1227 | DB 4 | Length 270 |
| Best Local Similarity | 85.2% | Pred. No. 4,1e-105 | | |
| Matches 230 | Conservative 16 | Mismatches 22 | Indels 2 | Gaps 1 |
| Qy | 27 | MFLALLGGLGCGVVCSTALFLYFRADMPNRISSEDTSCFYRLRLRHENADLDQSTLSE | 86 | |
| | | | | |
| Db | 1 | MFVALLLGGLGCGVVCVALFEYFRADMPNRISSEDTSCFYRLRLRHENADLDQSTLSE | 60 | |
| Qy | 87 | DT--LPDSCRMRKAFQGAVALQKELDHITGPRQFSGAPRMESGWTLDVQRGKPEADQRFH | 144 | |
| | | : | | |
| Db | 61 | DTKLIPDSCRRIKAFQGAVALQKELDHITGSHIIRKEMAVDSWIDLAKRSLEKQRFH | 120 | |
| Qy | 145 | LTINAATLPSGSHKVTLSWTYHRCMAKISNWTLSNGKLRYNQDGFYLLYANICFRNHET | 204 | |
| | | | | |
| Db | 121 | LTINATDIPSGSHKVSLSMYHRCMAKISNWTLSNGKLRYNQDGFYLLYANICFRNHET | 180 | |
| Qy | 205 | SGSVPTDILQALAVYVVKTSIKIPSSHNLMKGGSTKNMGSGSEFHHYSINVGGEFKLRAGE | 264 | |
| | | : | | |
| Db | 181 | SGDLATEYLQALAVYVVKTSIKIPSSHTLMKGGSTYVWGSNSEFHHYSINVGGEFKLRAGE | 240 | |
| Qy | 265 | EISIQVSNPSLLDPDQATYFGAKRYVDID | 294 | |
| | | | | |
| Db | 241 | EISIEVSNPSLLDPDQATYFGAKRYVDID | 270 | |

| RESULT | 5 | | |
|--------|---|--------------|--------------|
| ID | 09JUK8 | PRELIMINARY: | PRT: 199 AA. |
| AC | 09JUK8; | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Last sequence update) | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last annotation update) | | |
| DE | RECEPTOR ACTIVATOR OF NF-KB LIGAND 3. | | |
| GN | TNFSF11 OR RANKL 3. | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxId=10090; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=21150053; PubMed=11250921; | | |
| RA | Ikega T., Kasai M., Utsuyama M., Hirokawa K.; | | |
| RT | "Determination of three isoforms of the Receptor Activator of Nuclear | | |
| RT | Factor kappaB Ligand and Their Differential Expression in Bone and | | |
| RT | Thymus."; | | |
| RL | Endocrinology 142:1419-1426(2001). | | |
| DR | EMBL, AB032772; BAA97258.1; - | | |
| DR | HSSP, P50591; IDOG. | | |
| DR | MGI: 1100089; Tnfse11. | | |
| DR | InterPro: IPR0033263; TNF-5. | | |
| DR | InterPro: IPR003636; TNF-abc. | | |
| DR | InterPro: IPR000478; TNF_family. | | |
| DR | Pfam: PF00229; TNF; 1. | | |
| DR | ProDom: PD002012; TNF-abc; 1. | | |
| DR | ProDom: PD006600; TNF-5; 1. | | |
| DR | SMART: SM00207; TNF; 1. | | |
| DR | SMART: PS50049; TNF-2; 1. | | |
| DR | SEQUENCE 199 AA; 22150 MW; 401C13B5F8CE16 CRC64; | | |

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Query Match Summary: 67.7%; Score 1057; DB 11; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.3e-89;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 96 MKOAFQGAQVQKLEQIHVGPREFSGAPAMMEGSMLVDAQKGRKPEAOPFALLTTINASTIPSG 155
DB 1 MKOAFQGAQVQKLEQIHVGPREFSGAPAMMEGSMLVDAQKGRKPEAOPFALLTTINASTIPSG 60
QY 156 SKKVTLLSSVYHGRGMAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYLOL 215
DB 61 SKKVTLLSSVYHGRGMAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYLOL 120
QY 216 MYYVVKTSIKIPSSHNLMKSGSTKMMSCNSEPHFYSINVGCFEFKLRAGEISTIOVSNNPSL 275
DB 121 MYYVVKTSIKIPSSHNLMKSGSTKMMSCNSEPHFYSINVGCFEFKLRAGEISTIOVSNNPSL 180
QY 276 LDPDDDATYFEGAFKQVDDID 294
DB 181 LDPDDDATYFEGAFKQVDDID 199

RESULT 6
991219
ID Q91219 PRELIMINARY; PRT: 53 AA.
AC Q91219;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TMSF11 (FRAGMENT).
CN TMSF11..
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
XX NCBI_taxid=10116;
XX [1]
RN RA
RP SEQUENCE FROM N.A.
RC STRAIN=EF34;
RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C.A., Mason-Savas A.,
RA Saladi F.F., Popoff S.N., Lengner C., van Hul W., Choi Y., Marks S.C.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the Tmsf11 (TRANC, RANKL, ODF, OPG) gene.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF425669; AL23963.1; -.
FT NON_TER 1
SQ SEQUENCE 53 AA: 5876 MW: 8A71E32F2B6A9410 CRC64;

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| | | | | |
|-----------------------|--|---|-------|--------------------------------|
| Query Match | 17.4% | Score 272 | DB 11 | Length 53 |
| Best Local Similarity | 96.2% | Pred. No. 5.5e-18 | | |
| Matches | 51 | Conservative | 2 | Mismatches 0; Indels 0; Gaps 0 |
| QY | 242 | SGNSEHFHYSINVGSEFFKLAGEEISIIQVSNPSLLDPDODATYFGAFKQVOD | 294 | |
| | | | | |
| DB | 1 | SGNSEHFHYSINVGSEFFKLAGEEISIIQVSNPSLLDPDODATYFGAFKQVOD | 53 | |
| RESULT | 7 | | | |
| Q9DDZ5 | | PRELIMINARY | PRT: | 214 AA. |
| AC | Q9DDZ5 | | | |
| DT | 01-MAR-2001 | (TREMBLrel. 16, Created) | | |
| DT | 01-MAR-2001 | (TREMBLrel. 16, Last sequence update) | | |
| DT | 01-DEC-2001 | (TREMBLrel. 19, Last annotation update) | | |
| DE | TRAIL-LIKE PROTEIN. | | | |
| GN | TNSF10L | | | |
| OS | Brachydanio rerio (Zebrafish) (Zebra danio). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; | | | |
| OC | Cypriniformes; Cyprinidae; Danio. | | | |
| OX | NCBI_TaxID=7955; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |


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ID 09BDM3 PRELIMINARY; PRT; 261 AA.
AC 09BDM3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CD154 PROTEIN.
OS Aotus trilineatus (Night monkey) (Douroucoulli).
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344860; AAK37542.1; -.
DR HSSP; P29965; 1ALY.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SO SEQUENCE 261 AA; 29357 MW; 85E1588B507901B5 CRC64;

Query Match 11.6%; Score 180.5; DB 6; Length 261;
Best Local Similarity 26.3%; Pred. No. 1.4e-08;
Matches 77; Conservative 50; Mismatches 115; Indels 51; Gaps 16;

OY 10 PAPSPAPAPAPASRSNFLLLGLGIGVCSIALF-LYPRADMPPKRSSTHCFYR 68
DB 8 PAPRSAAAGLP-VSMKIFMYLLTFITQMIGSALFAVYLHRRLD-KIEDER----- 57
OY 69 ILRLHENDLDSTLESSEDTLPDS-----CRMQAQOGAVQKELQHVGPQRSGAPAM 123
DB 58 --NLHEDVPM-KTIQRKNTGERSLSLNCCEIRKSQFEGV-KDIM-----LNKEEK 106
OY 124 MEGSLDVAQGRKPEAPFAHLITNAISPSGSHKVTLSWYHGRMAKISN--MTLSNG 181
DB 107 KENSE--EMQKGDQNPQIAAHV-----ISEASSKTSVLOMAEKGYTSSNNLVTLENG 158
OY 182 K-LRVNODGFYLLANICF-RHNETSGSVPTDYQLMVAVYVKTSSHN--LMKGS 237
DB 159 KQLVKKGGLYTYAQVTFESNREASSQAP-----FLASLCLKPPNPFERILLRAAN 210
OY 238 TKMNSGSEFHFYSINVGGFKLKAGEISIOVNSPSSLRPPDDATYEGAFKV 290
DB 211 TH--SSAKPCQGSINHLGIFELDPGASVFNVDPSQVSHGTGFTSFGLLKL 261

RESULT 11
ID 09MYL6 PRELIMINARY; PRT; 280 AA.
AC 09MYL6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FAS LIGAND.
OS Macaca nemestrina (Pig-tailed macaque).
OS Macaca fascicularis (Crap eating macaque) (Cynomolus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cercopitheciinae; Macaca.
OC NCBI_TaxID=9545; 9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.

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RC SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY;
RA Kiril Y., Inoue T., Yoshino K.;
RT "Pig-called monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis; STRAIN=CYNOMOLUS MONKEY;
RA Kiril Y., Inoue T., Yoshino K.;
RT "Cynomolus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=RHEBUS MONKEY;
RA Kiril Y., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035140; BA90296.1; -.
DR EMBL; AB035138; BA90294.1; -.
DR EMBL; AB035139; BA90295.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SO SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 11.5%; Score 179; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 2.1e-08;
Matches 67; Conservative 45; Mismatches 102; Indels 92; Gaps 10;

OY 3 PHEGPLPAPSPAPAP--APPAASRS-----MFLALLIGLIGVCSIALF 46
DB 49 PRPPPLPRPPPLPRPLRLPKKRNHSTGLVMFPMVALVALGGLG-----MF 101
OY 47 LYPRADMPPKRSSTHCFYRLRLHENDLDSTLESSEDTLPDSCRMQAQOGAVOK 106
DB 102 QLFHLD-----KELAELESTYSQKHTA-----SLEK 128
OY 107 ELQHIYGPQFGSAPARMGSLDVAQGRKPEAPFAHLT--INASIPSGSHKVTLSW 164
DB 129 QIGHPPRPE-----KKDQRVAVHLTGKPNRSMP-----LEW 161
OY 165 YHGRMAKISNMTLSNGKLRVNODGFYLLANICFRHNETSGSVPTDYQLMVAVYVKTSS 224
DB 162 EDTYGVILLGVKKYKGGVLINETGLTFYYSKVYRQSGCTN-----LPLSHKVMNNS 215
OY 225 KIPSSHNLKMGKSTKNWSGSEFHFYSINVGGFKLKAGEISIOVNSPSSLRPPDDATY 284
DB 216 KYPQDLVME--GKMMSYCTTGQMAHSSYLGAVENTLSADHLVYVSELVNFEESTF 274
OY 285 FGAFKV 290
DB 275 FGLYKL 280

RESULT 12
ID 09BDM5 PRELIMINARY; PRT; 280 AA.
AC 09BDM5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

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OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RX SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344856; AAK37539.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR002965; P_rich_extensn.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PRO1217; PRICHEXTENS.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
SO SEQUENCE 280 AA; 31377 MW; 729EA61436F2D398 CRC64;

Query Match 11.3%; Score 177; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 3.1e-08;
Matches 67; Conservative 44; Mismatches 103; Indels 92; Gaps 10;

OY 3 PHEGRLPAPAPAP--APPAPASRS-----MFALLGLGIGVCSIALF 46
DB 49 PPPPLPPPPPLPLPLPLPKKGNHSTGLCLVFMFVALVALVGLG-----MF 101
OY 47 LYFRAQMDPNRISDSHCFYRLRLHENADLDSTLESDTLPDSCRMRKAFQAVOK 106
DB 102 QLFHLQ-----KELALRETSQKHTA-----SLEK 128
OY 107 ELQHTVGPFRSGAPAMEGSWLDVAQRKPEAPFAHLT--INAATPSGSHKVTLSW 164
DB 129 QIGHSPPE-----KKEQRKVAHLTGKPNRSMV-----LEW 161
OY 165 YHNRGAKISNMTLSNGKRLVNDGFFLYLANICFRHHETSGSVPTDYLQIMVYVYKTSI 224
DB 162 EDTYGIIVLSGVKKYKGGVLYNETGLTFYYSKYVFRGOSCTN-----LPLSHKYVRNS 215
OY 225 KIPSSHNLKMGSGTKNMSGNSEFFHYISINVGFFKLRAGEEISIOVSNPSLLDPDODATY 284
DB 216 KYPQDLVAME-GKMSYCTTGQMAHSSYLGAVFNLTSADHLVYVNSELSLVNEESOTF 274
OY 285 FGAFKV 290
DB 275 FGLYKL 280

RESULT 13
O9BDN1 PRELIMINARY; PRT; 280 AA.
AC O9BDN1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CD95L PROTEIN.
OS Cercocobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercocobus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules."
RL Immunogenetics 0:0-0(2001).

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RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344847; AAK37606.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR002965; P_rich_extensn.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PRO1217; PRICHEXTENS.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
SO SEQUENCE 280 AA; 31407 MW; 729EA60067BD398 CRC64;

Query Match 11.2%; Score 175; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 4.8e-08;
Matches 67; Conservative 44; Mismatches 103; Indels 92; Gaps 10;

OY 3 PHEGRLPAPAPAP--APPAPASRS-----MFALLGLGIGVCSIALF 46
DB 49 PPPPLPPPPPLPLPLPLPKKGNHSTGLCLVFMFVALVALVGLG-----MF 101
OY 47 LYFRAQMDPNRISDSHCFYRLRLHENADLDSTLESDTLPDSCRMRKAFQAVOK 106
DB 102 QLFHLQ-----KELALRETSQKHTA-----SLEK 128
OY 107 ELQHTVGPFRSGAPAMEGSWLDVAQRKPEAPFAHLT--INAATPSGSHKVTLSW 164
DB 129 QIGHSPPE-----KKEQRKVAHLTGKPNRSMV-----LEW 161
OY 165 YHNRGAKISNMTLSNGKRLVNDGFFLYLANICFRHHETSGSVPTDYLQIMVYVYKTSI 224
DB 162 EDTYGIIVLSGVKKYKGGVLYNETGLTFYYSKYVFRGOSCTN-----LPLSHKYVRNS 215
OY 225 KIPSSHNLKMGSGTKNMSGNSEFFHYISINVGFFKLRAGEEISIOVSNPSLLDPDODATY 284
DB 216 KYPQDLVAME-GKMSYCTTGQMAHSSYLGAVFNLTSADHLVYVNSELSLVNEESOTF 274
OY 285 FGAFKV 290
DB 275 FGLYKL 280

RESULT 14
O9BDC7 PRELIMINARY; PRT; 261 AA.
AC O9BDC7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CD154 PROTEIN.
OS Macaca mulatta (Rhesus macaque), and
OS Cercocobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544; 9531;
RN [1]
RP SEQUENCE FROM N.A.
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules."
RL Immunogenetics 0:0-0(2001).

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DR EMBL: AF344859; AAK37541.1; -
 DR EMBL: AF344841; AAK37600.1; -
 DR HSBP; P29965; 1ALY.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PSS0049; TNF_2; 1.
 DR VARIANT 60 60 H -> Q.
 DR VARIANT 204 204 I -> V.
 DR VARIANT 206 206 L -> P.
 DR VARIANT 215 215 A -> T.
 SO SEQUENCE 261 AA; 29366 MW; AA2E0F11C0F28ABB CRC64;

Query Match 11.2%; Score 174.5; DB 6; Length 261;
 Best Local Similarity 25.0%; Pred. No. 4,8e-08;
 Matches 73; Conservative 51; Mismatches 119; Indels 49; Gaps 15;

OY 10 PAPSADPAPAPPAASRSMFLALGLIGOVCSIALFLYFRQMDPNRISDSTHCFRI 69
 DB 8 PSPRSATATGLPYRMKIFMYLITFL-ITQMIGSALFAVYLHRRLD--KIEDR----- 57
 OY 70 LRLEHNAADLQDSTLESDTLPS-----GRMKAFQCAVQKELOHIVGPQRFSGAPAM 124
 DB 58 -NIHEDFVPM-KTQRCNTERSLSLNCEIKSQFEGFV-KDIM-----LNKEKKK 107
 OY 125 EGSMLDVAQRGPEAOPFAHLTINNASIPSGSHKVTLSWYHDSGMKISN--MTLSNGK 182
 DB 108 ENSF--EMQKGDQNPQIAHV-----ISEASKTTSVLQMAEKGYTMSNNLVTLENGK 159
 OY 183 -LRVNODGFYLYANICF-RHHTSGSVPTDYQLQMLVYVVKTSIKIPSSH--LMKGSST 238
 DB 160 QLTVKRGGLYLYAQTVECSNREASSQAP-----FIASLCKSPGRFERILLRAANT 211
 OY 239 KMWSCNSEFHFYSINVGFFKLRAGEEISIOVNSPLDPPDQATYFCAFKV 290
 DB 212 H--SSAKPCGQSIHLGCVFELQPGASVFNVTDPQVSHGCTGFTSGLKL 261

RESULT 15
 O95N10 PRELIMINARY; PRT; 282 AA.
 AC O95N10;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE PAS LIGAND.
 GN PASL.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhu N., Young Y.;
 RT "Molecular cloning and characterization of porcine Pas ligand cDNA";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY033634; AAK56449.1; -
 SO SEQUENCE 282 AA; 31752 MW; F391212406AE1E7D CRC64;

Query Match 11.1%; Score 173; DB 6; Length 282;
 Best Local Similarity 21.6%; Pred. No. 7,4e-08;
 Matches 66; Conservative 45; Mismatches 102; Indels 92; Gaps 10;

OY 3 PHEGRLPAPASAPAPPAASNS-----MFLALGLIGOVCSIALFL 47
 DB 53 PPPPLLPSPRLP-PLPPSLKKRKHINAGLCLLVFMFVALVGLGLG-----MFG 104
 OY 48 YFRAQMDPNRISDSTHCFYRLRLHENDLQDSTLESDTLPSDSCRMKAFQCAVQKE 107

DB 105 LFHLQKE-----LTELRESASORHT-----ESSLEKQ 131
 OY 108 LOHIVGPQRFSGAPAMMEGSMLDVAQRGKPEAOPFAHLT--INNASIPSGSHKVTLSWY 165
 DB 132 IGHPLPSE-----KKELRKVAHLTGKPNRSRIP-----LEWE 164
 OY 166 HDRCAKISNMTLNSGKLVRNODGFYLYANICFRHHETSGSVPTDYQLQMLVYVVKTSIK 225
 DB 165 DTYGIALVSGVYKMGSLVINDTGLYFYSKVYFRGVCNNQ-----PLSHKYTTNSR 218
 OY 226 IPPSHNLKMGSGSTKMWSCNSEFHFYSINVGFFKLRAGEEISIOVNSPLDPPDQATYF 285
 DB 219 YPQDLVLM-E-GKMMNYCTTGQMMARSSYLGAVFNLTSADHLVYVNSLSLVNFEESKTF 277
 OY 286 GAFKY 290
 DB 278 GLYKL 282

Search completed: July 8, 2002, 19:52:38
 Job time: 12582 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 23:50:08 : Search time 4715.96 Seconds
(without alignments)
4233.267 Million cell updates/sec

Title: US-09-865-363-12

Perfect score: 954
Sequence: 1 ATGCGCGCGCGCCAGACAGA.....AAGTTCGAGATATAGATTGA 954

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hngo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
|------------|-------|-------------|--------|-------|-------------|

| | | | | | | |
|----|-------|-------|--------|----|------------|--------------------|
| 1 | 954 | 100.0 | 954 | 6 | AR156434 | AR156434 Sequence |
| 2 | 954 | 100.0 | 954 | 6 | AR164148 | AR164148 Sequence |
| 3 | 954 | 100.0 | 954 | 6 | AX147989 | AX147989 Sequence |
| 4 | 954 | 100.0 | 1034 | 9 | AB064269 | AB064269 Homo sapi |
| 5 | 954 | 100.0 | 2201 | 9 | AF019047 | AF019047 Homo sapi |
| 6 | 954 | 100.0 | 2271 | 9 | AF053712 | AF053712 Homo sapi |
| 7 | 858 | 89.9 | 911 | 9 | AB064227 | AB064227 Homo sapi |
| 8 | 822.2 | 86.2 | 972 | 9 | AB064270 | AB064270 Homo sapi |
| 9 | 790 | 82.8 | 818 | 9 | AB064268 | AB064268 Homo sapi |
| 10 | 739 | 77.5 | 930 | 6 | AB037599 | AB037599 Homo sapi |
| 11 | 733.2 | 76.9 | 1823 | 9 | AX201362 | AX201362 Sequence |
| 12 | 675.4 | 70.8 | 957 | 10 | AF187319 | AF187319 Homo sapi |
| 13 | 666.2 | 69.8 | 951 | 6 | AF019048 | AF019048 Mus muscu |
| 14 | 666.2 | 69.8 | 951 | 6 | E34350 | E34350 DNA and pro |
| 15 | 666.2 | 69.8 | 951 | 6 | E36388 | E36388 Novel prote |
| 16 | 666.2 | 69.8 | 951 | 10 | AB008426 | AB008426 Mus muscu |
| 17 | 666.2 | 69.8 | 951 | 10 | AB036798 | AB036798 Mus muscu |
| 18 | 666.2 | 69.8 | 2191 | 6 | AR157058 | AR157058 Sequence |
| 19 | 666.2 | 69.8 | 2191 | 6 | AX140162 | AX140162 Sequence |
| 20 | 666.2 | 69.8 | 2295 | 6 | AR062119 | AR062119 Sequence |
| 21 | 666.2 | 69.8 | 2239 | 10 | AF053713 | AF053713 Mus muscu |
| 22 | 666.2 | 69.8 | 2237 | 10 | AF013170 | AF013170 Mus muscu |
| 23 | 663 | 69.5 | 1630 | 6 | AR156433 | AR156433 Sequence |
| 24 | 615 | 64.5 | 1630 | 6 | AR164147 | AR164147 Sequence |
| 25 | 615 | 64.5 | 1630 | 6 | AX147987 | AX147987 Sequence |
| 26 | 615 | 64.5 | 1630 | 6 | AB032771 | AB032771 Mus muscu |
| 27 | 591.8 | 62.0 | 864 | 10 | AB032772 | AB032772 Mus muscu |
| 28 | 511.6 | 53.6 | 754 | 10 | AC023297 | AC023297 Homo sapi |
| 29 | 425 | 44.5 | 113451 | 2 | AL139382 | AL139382 Human DNA |
| 30 | 425 | 44.5 | 200724 | 9 | AX232589 | AX232589 Sequence |
| 31 | 365.6 | 38.3 | 522 | 6 | AC094149 | AC094149 Rattus no |
| 32 | 327 | 34.3 | 123551 | 2 | E34349 | E34349 DNA and pro |
| 33 | 325.4 | 34.1 | 2029 | 6 | AB022036S4 | AB022036 Mus muscu |
| 34 | 325.4 | 34.1 | 2029 | 10 | AB022036S1 | AB022036 Mus muscu |
| 35 | 153 | 16.0 | 764 | 10 | E34346 | E34346 DNA and pro |
| 36 | 151.4 | 15.9 | 2026 | 6 | AC094149 | AC094149 Rattus no |
| 37 | 126.6 | 13.3 | 123551 | 2 | AC104794 | AC104794 Homo sapi |
| 38 | 125.4 | 13.1 | 161835 | 2 | AC010969 | AC010969 Homo sapi |
| 39 | 125.4 | 13.1 | 190748 | 9 | AF425669 | AF425669 Rattus no |
| 40 | 124 | 13.0 | 809 | 10 | E34347 | E34347 DNA and pro |
| 41 | 114.2 | 12.0 | 468 | 6 | AB022036S2 | AB022037 Mus muscu |
| 42 | 114.2 | 12.0 | 468 | 10 | AC023297 | AC023297 Homo sapi |
| 43 | 104.2 | 7.9 | 113451 | 2 | AC016938 | AC016938 Homo sapi |
| 44 | 71 | 7.4 | 157943 | 2 | AC007051 | AC007051 Homo sapi |
| 45 | 71 | 7.4 | 167810 | 9 | | |

ALIGNMENTS

| | | | | | |
|------------|--|-------------|-----|--------|-----------------|
| RESULT 1 | AR156434 | 954 bp | DNA | linear | PAT 08-AUG-2001 |
| LOCUS | AR156434 | | | | |
| DEFINITION | Sequence 12 from patent US 6242213. | | | | |
| ACCESSION | AR156434 | | | | |
| VERSION | AR156434.1 | GI:15125138 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | Unclassified. | | | | |
| AUTHORS | 1 (bases 1 to 954) | | | | |
| TITLE | Anderson,D.M. | | | | |
| JOURNAL | Isolated DNA molecules encoding RANK-L | | | | |
| FEATURES | Patent: US 6242213-A 12 05-JUN-2001; | | | | |
| source | Location/Qualifiers | | | | |
| | 1..954 | | | | |
| | /organism="unknown" | | | | |
| BASE COUNT | 255 a 239 c 227 g 233 t | | | | |
| ORIGIN | | | | | |

Query Match 100.0%; Score 954; DB 6; Length 954;
Best Local Similarity 100.0%; Pred. No. 5,6e-188;

| Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
|--|-----|--|-----|--|--|--|--|--|--|
| QY | 1 | ATGCGCGCGCCAGACAGACTACACAACTACTGCTGCTGCGAGAGATGGGCGC | 60 | | | | | | |
| DB | 1 | ATGCGCGCGCCAGACAGACTACACAACTACTGCTGCTGCGAGAGATGGGCGC | 60 | | | | | | |
| QY | 61 | GGCGCGGAGCGCGCGAGAGGGGCCCCCTGCACGCCCCGCGCGCTGGCGCAG | 120 | | | | | | |
| DB | 61 | GGCGCGGAGCGCGCGAGAGGGGCCCCCTGCACGCCCCGCGCGCTGGCGCAG | 120 | | | | | | |
| QY | 121 | CCCCCGCGCGCTCCGCTCCATGTCGTGCGCTGCGGCTGGGCGCTGGGCGAGTT | 180 | | | | | | |
| DB | 121 | CCCCCGCGCGCTCCGCTCCATGTCGTGCGCTGCGGCTGGGCGCTGGGCGAGTT | 180 | | | | | | |
| QY | 181 | GTCGACAGCGTCCGCTGCTTCTATTTTCAGAGCGAGATGGATTCCTAATAGATATCA | 240 | | | | | | |
| DB | 181 | GTCGACAGCGTCCGCTGCTTCTATTTTCAGAGCGAGATGGATTCCTAATAGATATCA | 240 | | | | | | |
| QY | 241 | GAAGATGGCACTCACTGATTTATAGAAATTTGAGACTCCATGAATAATGCAGATTTTCAA | 300 | | | | | | |
| DB | 241 | GAAGATGGCACTCACTGATTTATAGAAATTTGAGACTCCATGAATAATGCAGATTTTCAA | 300 | | | | | | |
| QY | 301 | GACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATTCATGAGAGATTTAA | 360 | | | | | | |
| DB | 301 | GACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATTCATGAGAGATTTAA | 360 | | | | | | |
| QY | 361 | CAGGCTTTCAAGAGAGCTGTGCAAAAGGAATTAACATATCGTTGGATCTCAGACATC | 420 | | | | | | |
| DB | 361 | CAGGCTTTCAAGAGAGCTGTGCAAAAGGAATTAACATATCGTTGGATCTCAGACATC | 420 | | | | | | |
| QY | 421 | AGACAGAGAAAGGAGTGGATGGCTCATGTTAGATCTGGCCAGAGAGAGCAAGCTT | 480 | | | | | | |
| DB | 421 | AGACAGAGAAAGGAGTGGATGGCTCATGTTAGATCTGGCCAGAGAGAGCAAGCTT | 480 | | | | | | |
| QY | 481 | GAAGCTCAGCCTTTGCTCATCTCACTATTAATGCGACCGACATCCCATCTGTTCCCAT | 540 | | | | | | |
| DB | 481 | GAAGCTCAGCCTTTGCTCATCTCACTATTAATGCGACCGACATCCCATCTGTTCCCAT | 540 | | | | | | |
| QY | 541 | AAAGGAGTCTGCTCTGTTGACCATGATGGGGTTGGGCGAAGATCTCCAACTGACT | 600 | | | | | | |
| DB | 541 | AAAGGAGTCTGCTCTGTTGACCATGATGGGGTTGGGCGAAGATCTCCAACTGACT | 600 | | | | | | |
| QY | 601 | TTTACCAATGGAATACTAATAGTTAATCAGATGGCTTTTATACCTGTATGCCAATTT | 660 | | | | | | |
| DB | 601 | TTTACCAATGGAATACTAATAGTTAATCAGATGGCTTTTATACCTGTATGCCAATTT | 660 | | | | | | |
| QY | 661 | TGCTTTGCACATCATGAATACTCAGAGACCTAGCTACAGAGTATCTCACTAATGCTG | 720 | | | | | | |
| DB | 661 | TGCTTTGCACATCATGAATACTCAGAGACCTAGCTACAGAGTATCTCACTAATGCTG | 720 | | | | | | |
| QY | 721 | TACGTCACCTAAACAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAGAGGAAGC | 780 | | | | | | |
| DB | 721 | TACGTCACCTAAACAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAGAGGAAGC | 780 | | | | | | |
| QY | 781 | ACCAAGTATTTGTCAGGGAAATTCGAATTTCAATTTTATTCATTAAGGTTGATGAT | 840 | | | | | | |
| DB | 781 | ACCAAGTATTTGTCAGGGAAATTCGAATTTCAATTTTATTCATTAAGGTTGATGAT | 840 | | | | | | |
| QY | 841 | TTTAAGTTACGGTCTGGAGAGAAATCAGATCGAGGTCCTCAACCCCTCTACTGAT | 900 | | | | | | |
| DB | 841 | TTTAAGTTACGGTCTGGAGAGAAATCAGATCGAGGTCCTCAACCCCTCTACTGAT | 900 | | | | | | |
| QY | 901 | CCGATTCAGAGATGCAACATCTTTGGGGCTTTTAAAGTTCGAGATATAGATTGA | 954 | | | | | | |
| DB | 901 | CCGATTCAGAGATGCAACATCTTTGGGGCTTTTAAAGTTCGAGATATAGATTGA | 954 | | | | | | |

| KEYWORDS | | | | | | | | | |
|--|-----|--|-----|--|--|--|--|--|--|
| SOURCE | | | | | | | | | |
| ORGANISM | | | | | | | | | |
| REFERENCE | | | | | | | | | |
| AUTHORS | | | | | | | | | |
| TITLE | | | | | | | | | |
| JOURNAL | | | | | | | | | |
| FEATURES | | | | | | | | | |
| source | | | | | | | | | |
| BASE COUNT | | | | | | | | | |
| ORIGIN | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity | | | | | | | | | |
| Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | ATGCGCGCGCCAGACAGACTACACAACTACTGCTGCTGCGAGAGATGGGCGC | 60 | | | | | | |
| DB | 1 | ATGCGCGCGCCAGACAGACTACACAACTACTGCTGCTGCGAGAGATGGGCGC | 60 | | | | | | |
| QY | 61 | GGCGCGGAGCGCGCGAGAGGGGCCCCCTGCACGCCCCGCGCGCTGGCGCAG | 120 | | | | | | |
| DB | 61 | GGCGCGGAGCGCGCGAGAGGGGCCCCCTGCACGCCCCGCGCGCTGGCGCAG | 120 | | | | | | |
| QY | 121 | CCCCCGCGCGCTCCGCTCCATGTCGTGCGCTGCGGCTGGGCGCTGGGCGAGTT | 180 | | | | | | |
| DB | 121 | CCCCCGCGCGCTCCGCTCCATGTCGTGCGCTGCGGCTGGGCGCTGGGCGAGTT | 180 | | | | | | |
| QY | 181 | GTCGACAGCGTCCGCTGCTTCTATTTTCAGAGCGAGATGGATTCCTAATAGATATCA | 240 | | | | | | |
| DB | 181 | GTCGACAGCGTCCGCTGCTTCTATTTTCAGAGCGAGATGGATTCCTAATAGATATCA | 240 | | | | | | |
| QY | 241 | GAAGATGGCACTCACTGATTTATAGAAATTTGAGACTCCATGAATAATGCAGATTTTCAA | 300 | | | | | | |
| DB | 241 | GAAGATGGCACTCACTGATTTATAGAAATTTGAGACTCCATGAATAATGCAGATTTTCAA | 300 | | | | | | |
| QY | 301 | GACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATTCATGAGAGATTTAA | 360 | | | | | | |
| DB | 301 | GACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATTCATGAGAGATTTAA | 360 | | | | | | |
| QY | 361 | CAGGCTTTCAAGAGAGCTGTGCAAAAGGAATTAACATATCGTTGGATCTCAGACATC | 420 | | | | | | |
| DB | 361 | CAGGCTTTCAAGAGAGCTGTGCAAAAGGAATTAACATATCGTTGGATCTCAGACATC | 420 | | | | | | |
| QY | 421 | AGACAGAGAAAGGAGTGGATGGCTCATGTTAGATCTGGCCAGAGAGAGCAAGCTT | 480 | | | | | | |
| DB | 421 | AGACAGAGAAAGGAGTGGATGGCTCATGTTAGATCTGGCCAGAGAGAGCAAGCTT | 480 | | | | | | |
| QY | 481 | GAAGCTCAGCCTTTGCTCATCTCACTATTAATGCGACCGACATCCCATCTGTTCCCAT | 540 | | | | | | |
| DB | 481 | GAAGCTCAGCCTTTGCTCATCTCACTATTAATGCGACCGACATCCCATCTGTTCCCAT | 540 | | | | | | |
| QY | 541 | AAAGGAGTCTGCTCTGTTGACCATGATGGGGTTGGGCGAAGATCTCCAACTGACT | 600 | | | | | | |
| DB | 541 | AAAGGAGTCTGCTCTGTTGACCATGATGGGGTTGGGCGAAGATCTCCAACTGACT | 600 | | | | | | |
| QY | 601 | TTTACCAATGGAATACTAATAGTTAATCAGATGGCTTTTATACCTGTATGCCAATTT | 660 | | | | | | |
| DB | 601 | TTTACCAATGGAATACTAATAGTTAATCAGATGGCTTTTATACCTGTATGCCAATTT | 660 | | | | | | |
| QY | 661 | TGCTTTGCACATCATGAATACTCAGAGACCTAGCTACAGAGTATCTCACTAATGCTG | 720 | | | | | | |
| DB | 661 | TGCTTTGCACATCATGAATACTCAGAGACCTAGCTACAGAGTATCTCACTAATGCTG | 720 | | | | | | |
| QY | 721 | TACGTCACCTAAACAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAGAGGAAGC | 780 | | | | | | |
| DB | 721 | TACGTCACCTAAACAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAGAGGAAGC | 780 | | | | | | |
| QY | 781 | ACCAAGTATTTGTCAGGGAAATTCGAATTTCAATTTTATTCATTAAGGTTGATGAT | 840 | | | | | | |

Db 781 ACCAACTATTGCTCAGGAAATTCGAAATTCATTTTATTCATMAACCTGTGGATTT 840

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Qy 901 CCGGATCAGAGATGCAACATCTTTGGGCTTTTAAAGTTGAGATATGATTTGA 954
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RESULT 3

AX147989 954 bp DNA linear PAT 08-JUN-2001

LOCUS AX147989 12 from Patent WO0136637.

DEFINITION AX147989

ACCESSION AX147989

VERSION AX147989.1 GI:14346964

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 954)

AUTHORS Anderson D.M. and Hughes,A.E.

TITLE Receptor activator of nf-kappa b

JOURNAL Patent: WO 0136637-A 12 25-MAY-2001;

FEATURES

source location/Qualifiers

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BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

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RESULT 4

AB064269 1034 bp mRNA linear PRI 26-DEC-2001

LOCUS AB064269

DEFINITION Homo sapiens hRANKL 1 mRNA for receptor activator of nuclear factor kappa B ligand 1, complete cds.

ACCESSION AB064269

VERSION AB064269.1 GI:18143618

KEYWORDS

SOURCE Homo sapiens cDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (sites)

AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.

TITLE Determination of human RANKL isoforms

JOURNAL Unpublished

2 (bases 1 to 1034)

AUTHORS Ikeda,T. and Kuroyama,H.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:tohru.plh2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)

FEATURES

source location/Qualifiers

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81..1034

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Best Local Similarity 100.0%; Pred. No. 5,7e-188;
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RESULT 5
AF019047      2201 bp      mRNA      linear      PRI 22-NOV-1997
LOCUS
DEFINITION
Homo sapiens receptor activator of nuclear factor kappa B ligand
ACCESSION
AF019047
VERSION
AF019047.1 GI:2612921
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2201)
Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Rometsko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
Galibert,L.
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
Nature 390 (656), 175-179 (1997)
98032977
MEDLINE
2 (bases 1 to 2201)
Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., Dubose,R. and Galibert,L.
Direct Submission
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
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LOCUS Homo sapiens osteoprotegerin ligand mRNA, complete cds.
DEFINITION AF053712
ACCESSION AF053712
VERSION AF053712.1 GI:3057145
KEYWORDS human.
ORGANISM Homo sapiens
SOURCE Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
REFERENCE 1 (bases 1 to 2271)
Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,

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Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Smeal, G., Guo, J.,
Delaney, J. and Boyle, W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle, W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
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RESULT 7

AB061227 911 bp mRNA linear PRI 03-NOV-2001
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DEFINITION Homo sapiens mRNA for hRANKL 2, complete cds.
ACCESSION AB061227
VERSION AB061227.1 GI:16610212
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (sites)
AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE Human RANKL isoform
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 911)
AUTHORS Ikeda,T. and Kuroyama,H.
JOURNAL Direct Submission
TITLE Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical
and Dental University, Pathology and Immunology; 1-5-45 Yushima,
Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:tohru.phn2@med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)

FEATURES

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BASE COUNT 253 a 211 c 217 g 230 t
ORIGIN

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Best Local Similarity 95.5%; Pred. No. 4.6e-168;
Matches 911; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

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RESULT 8

AB064270 972 bp mRNA linear PRI 26-DEC-2001
LOCUS AB064270
DEFINITION Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear
factor kappa B ligand 2-2, complete cds.
ACCESSION AB064270
VERSION AB064270.1 GI:18143620

KEYWORDS Homo sapiens cDNA to mRNA.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE Determination of human RANKL isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 972)
AUTHORS Ikeda,T. and Kuroyama,H.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail: toru.ph2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES
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Matches 827; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 9
AB064268 818 bp mRNA linear PRI 26-DEC-2001
LOCUS
DEFINITION Homo sapiens hRANKL 3 mRNA for receptor activator of nuclear factor kappa B ligand 3, complete cds.
ACCESSION AB064268
VERSION AB064268.1 GI:18143616
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE Determination of human RANKL isoforms
JOURNAL Unpublished
AUTHORS Ikeda,T. and Kuroyama,H.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail: toru.ph2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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RESULT 10

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DEFINITION AB037599.1 GI:6863047
ACCESSION
VERSION
KEYWORDS
SOURCE
cell_line:SCC-4 CDNA to mRNA.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (sites)
AUTHORS Nagai,M., Kyakumoto,S. and Sato,N.
TITLE Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation

JOURNAL Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)
MEDLINE 20175237
REFERENCE 2 (bases 1 to 930)
AUTHORS Nagai,M., Kyakumoto,S. and Sato,N.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry, 19-1 Uchiyama, Morioka, Iwate 020-8505, Japan (E-mail:mngai@iwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)

FEATURES

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ORIGIN

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| Qy | 756 | TCATACCTGATGAAAGAGGAAAGCAACAGATTTGGTCAGGAAATTCGATTCATTT | 815 |
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| Db | 691 | TTATTCATTAACGTTGGTGGATTTTTAACTTACGCTGTGAGAGGAAATCAGACATCGA | 750 |
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| ACCESSION | AX201362 | | PAT 30-AUG-2001 |
| VERSION | AX201362.1 | GI:15391175 | |
| KEYWORDS | human. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 2390) | | |
| AUTHORS | Ashtkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J., Piltl, R.M., Roy, M.A., Smith, V., Stone, D.M., Watanabe, C.K. and Wood, W.I. | | |
| TITLE | Compositions and methods for the treatment of tumor | | |
| JOURNAL | Patent: WO 0153486-A 41 26-JUL-2001; | | |
| FEATURES | GeneTech, Inc. (US) | | |
| source | 1..2390 | | |
| BASE COUNT | 778 a 417 c 506 g 688 t | | 1 others |
| ORIGIN | | | |
| Query Match | 77.5%: Score 739: DB 6: Length 2390: | | |
| Best Local Similarity | 100.0%: Pred. No. 2,5e-143: | | |
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BASE COUNT 569 a 305 c 380 g 569 t
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Query Match 76.9%; Score 733.2; DB 9; Length 1823;
 Best Local Similarity 99.6%; Pred. No. 3.9e-142;
 Matches 735; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 QY 757 CATACCTGATGAAAG 816
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 QY 937 GTTCGAGATATAGATTGA 954
 DB 721 GTTCGAGATATAGATTGA 738

RESULT 13
 AF187319 957 bp mRNA linear ROD 17-NOV-2000
 LOCUS
 DEFINITION Rattus norvegicus receptor activator of NF-kB ligand mRNA, complete
 cds
 ACCESSION AF187319
 VERSION AF187319.1 GI:10441420
 KEYWORDS

SOURCE
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 Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE
 1 (bases 1 to 957)
 Xu, J., Tan, J.W., Huang, L., Gao, X.H., Laird, R., Liu, D., Wysocki, S.
 and Zheng, M.H.
 Cloning, sequencing, and functional characterization of the rat
 homologue of receptor activator of NF-kappaB ligand
 J. Bone Miner. Res. 15 (11), 2178-2186 (2000)
 REFERENCE
 2 (bases 1 to 957)
 Xu, J.K. and Zheng, M.H.
 Direct Submission
 Submitted (16-SEP-1999) Orthopaedic Surgery, The University of
 Western Australia, Monash Ave., Nedlands, WA 6009, Australia
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 PEQPFALHTINADIPSGSHKYSLSWYHDGWMKRIKISNMTFSNKLIVNDGEFYLL
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BASE COUNT 230 a 260 c 256 g 211 t
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 Best Local Similarity 82.3%; Pred. No. 3.6e-130;
 Matches 788; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

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 DB 61 TCGCCGAGAGCCCGCAGAGAGGCGCCCTGCA--CGCCCGCGCGCTGCGCCGAC 120
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 DB 121 CCGCCCGCGCGCGCTCCGCTCCATGTTGCGTGGGCGCTCGGGGCTGGGCGCCAG 180
 QY 178 GTTGTGAGCGGTGCGCCCTGTTCTTATTTACAGAGCGCAGATGATCTTAATGAATA 237
 DB 181 GTTGTGAGCGGTGCGCCCTGTTCTTATTTACAGAGCGCAGATGATCTTAATGAATA 240
 QY 238 TCAGAGATGAGCACTCAGCATTTATAGATTTGAGACTCCAGAAATGCAATTTT 297
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 QY 298 CAGACACACACTGTGAGAGTCAAGATACAAATTAATCTGATTCATGTAGAGAAAT 357
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 DB 421 TTCTCAGAGAGTTCCAGCTATGATGAGAGGTTGCTGCTGATGTGGCCCGCGGCGGCAAG 480

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| Db | 481 | CCTGAGGCTCAACCCCTTTTGCTACTCTACACATCAATATGCTCCGGAATCCCACTGGGGTTCC | 540 |
| Oy | 538 | CATAAAGTAGATCTGTCTCCTTGGTAGCATGATCGGGGTTGGGCCAAGATCTCCAAATG | 597 |
| Db | 541 | CATAAAGTCAGTCTGTCTCCTTGGTAGCATGATCGAGGCTGGGCCAAGATCTCTAATG | 600 |
| Oy | 598 | ACTTTTACCAATGGAATACTAATTAATCAAGATGGCTTTTATTACTGTATGCCAAC | 657 |
| Db | 601 | ACGTTTAACCAACGGAAACTAAGGGTTAAACCAAGATGGCTTTTATTACTGTATGCCAAC | 660 |
| Oy | 658 | ATTGCTTTCCACATCATGAATACTTCAGAGAGACTAGCTACAGAGATCTTCAACTAATG | 717 |
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| Db | 781 | AGCACTTAAGAACTGGTCAAGGGGAATTCGATAATTCCTTTATTCATTAACCTTGAGAGA | 840 |
| Oy | 838 | TTTTTTTAAAGTTACGGTCTGAGAGAGGAATAACGACATCGAGGTCTCCAAACCCCTCTTACG | 897 |
| Db | 841 | TTTTTCAAGCTCCGGGCTGGTGAGGAATAATAGCGTCCAGGGTCCCAACCCCTTCCGTGG | 900 |
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RESULT 14
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DEFINITION    Mus musculus receptor activator of nuclear factor kappa B ligand
               (RANKL) mRNA, complete cds.
ACCESSION     AF019048
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2225)
Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometenko,D.M., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
Galibert,L.
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
Nature 390 (6656), 175-179 (1997)
98032977
2 (bases 1 to 2225)
Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., Dubose,R. and Galibert,L.
Direct Submission
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
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| QY | 61 | GGCCCCGGAGCGCCGACAGAGAGGCCCCCTGGACCGCCCCG | 117 | | | | | |
| Db | 197 | GGCCCCGGCGTCCACACAGAGAGGTCGGGTGACCCCGGCTTTCGACCGCGCTCGCGC | 256 | | | | | |
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| QY | 178 | GTTGCTGTGACGCGTGGCGCTGTTCTTCTATTTCAGAGCGGAGATGATCTTAATAGATA | 237 | | | | | |
| Db | 317 | GTTGCTGTGACGCGTGGCGCTGTTCTTCTATTTCAGAGCGGAGATGATCTTAATAGATA | 376 | | | | | |
| QY | 238 | TCAGAAAGTGTGGCAGCTGCTGATTTATAGAAATTTTGAACATCCATGAAATAGCAGATTTT | 297 | | | | | |
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| QY | 298 | CAAGACACAGCTGTGGAGATCAAGATACAAATTAATACCTGATTCATGTAGAGAAATTG | 357 | | | | | |
| Db | 437 | CAGAGCTGAGCTGTGGAGATGAGAGTGAAGACAC-----ACTACCTGACTCCTGCAGAGAGATG | 490 | | | | | |
| QY | 358 | AAACAGGCGCTTTCAGAGAGCTGTGCAAAAGAAATTAACAATATTCGTTGATACAGCAC | 417 | | | | | |
| Db | 491 | AAACAGGCGCTTTCAGAGAGGCGCGTGTGAGAAAGAACTGCAACATTTGTGGGCGACAGCGC | 550 | | | | | |
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| Db | 671 | CATAAAGTACGCTGTCTCTCTGTTGATACCATGATCGGGGTTGGGCCAAGATCTCTCAACATG | 730 | | | | | |
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| Db | 731 | ACGTTAAGCAACGGAACCTAAGGTTTAAACCAAGATGCTCTATTACCTGTAGCCCAAC | 790 | | | | | |
| QY | 658 | ATTTCGCTTTCGACATCAAGAACTTCACAGAACCTAGTACAGAGTATCTTCACTCAATATG | 717 | | | | | |
| Db | 791 | ATTTCGCTTTCGCGCATCAAGAACTTCGGAAGCGGTACCTACAGACTAATCTTCAGCTGATG | 850 | | | | | |
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| Db | 971 | TTTTTCAAGGCTCCAGGCTGTGGAAGAAATTTGACATTCAGGCTGTCCAAACCTTCCTCCTG | 1030 | | | | | |

QY 898 GATCCGATCGATGCAACATACCTTTGGGCTTTTAAAGTTCCAGATATAGATTGA 954
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LOCUS E34350
DEFINITION DNA and process for producing protein by using the same.
ACCESSION E34350.1 GI:18624335
VERSION JP 2000102390-A/5.
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 951)
AUTHORS Mizuno,A., Kodaira,K. and Kodaira,Y.
TITLE DNA and process for producing protein by using the same
JOURNAL Patent: JP 2000102390-A 5 11-APR-2000;
SNOW BRAND MILK PROD CO LTD,YS NEW TECHNOLOGY LAB
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PN JP 2000102390-A/5
PD 11-APR-2000
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Best Local Similarity 82.5%; Pred. No. 2.9e-128;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;
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Job time: 13458 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 21:43:41 ; Search time 408.13 Seconds

(without alignments)
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Searched: 1736436 seqs, 858457221 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 13 | 666.2 | 69.8 | 951 | 21 | AAAB9156 | Mouse OBM nucleot |
| 14 | 666.2 | 69.8 | 951 | 21 | AAAZ9965 | DNA encoding a mur |
| 15 | 666.2 | 69.8 | 951 | 21 | AAZ49024 | Osteoclast format |
| 16 | 666.2 | 69.8 | 1538 | 19 | AAAB9886 | Nucleic acid encod |
| 17 | 666.2 | 69.8 | 2191 | 19 | AAVA1489 | Nucleotide sequenc |
| 18 | 666.2 | 69.8 | 2295 | 19 | AAV70284 | Human osteoprotege |
| 19 | 666.2 | 69.8 | 2299 | 21 | AAZ99966 | DNA encoding a mur |
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| 21 | 615 | 64.5 | 1630 | 19 | AAVA1377 | NF-KB receptor act |
| 22 | 615 | 64.5 | 1630 | 19 | AAVA1371 | Murine receptor ac |
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| 29 | 325.4 | 34.1 | 2029 | 21 | AAAB9155 | DNA encoding osteo |
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| 39 | 114.2 | 12.0 | 468 | 21 | AAAB9153 | Human tumor necro |
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| 43 | 69.4 | 7.3 | 759 | 22 | AAAB3898 | GH-derived leader |
| 44 | 69.4 | 7.3 | 768 | 22 | AAAB8399 | CMV-derived leader |
| 45 | 69.4 | 7.3 | 801 | 22 | AAAD03112 | Ompa signal peptid |

ALIGNMENTS

| | |
|----------|--|
| RESULT | 1 |
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| ID | AAVA1378 |
| XX | XX |
| AC | AAVA1378: |
| XX | XX |
| DT | 08-OCT-1998 (first entry) |
| DE | NF-KB receptor activator RANK ligand (RANKL) encoding cDNA. |
| XX | XX |
| XX | RANK; necrosis factor-kappa B; NF-KB; receptor activator; human; |
| KW | Immune response; inflammatory response; toxic shock; sepsis; |
| KM | RANKL; RANK ligand; tumor necrosis factor; TNF; ss. |
| XX | XX |
| OS | Homo sapiens. |
| XX | XX |
| FH | Key |
| FT | CDS |
| FT | 1..954 |
| FT | /tag= a |
| XX | /product= "human RANKL (ligand for RANK)" |
| PN | W09828426-A2. |
| XX | XX |
| PD | 02-JUL-1998. |
| XX | XX |
| PF | 22-DEC-1997; 97WO-US23775. |
| XX | XX |
| PR | 14-OCT-1997; 97US-0064671. |
| PR | 23-DEC-1996; 96US-0059978. |
| PR | 07-MAR-1997; 97US-0813509. |
| XX | XX |
| PA | (IMMV) IMMUNEX CORP. |

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI: 1998-377657/32.

DR P-PSDB; AAM69957.

XX New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells

XX Claim 25; Pages 59-60; 80pp; English.

XX This CDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappa (NF-kb)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kb, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kb by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

XX Query Match 100.0%; Score 954; DB 19; Length 954;

XX Best Local Similarity 100.0%; Pred. No. 5e-241;

XX Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCGCGCCAGAGAGACTACACCAAGTACCTGCTGCTGAGAGATGGCGGC 60
DB 1 atgcgcgcgccagagagactaccacagtlacctgctgctgagagagatggcggc 60
QY 61 GGCCTCGGAGCCCGCAGACAGGCGCCCTGCGAGCGCCGCGCGCTGGCGCCAG 120
DB 61 ggcctcgagagcccgagagagagagagagagagagagagagagagagagagag 120
QY 121 CCCCCCGCGCTCCGCTCCATGTTGTTGCGCCCTCTGGGCGCTGGGCGCAGGTT 180
DB 121 ccccccgcgctccgctccatgttgcgtccctctggtggcgctggcgccaggtt 180
QY 181 GTCTGAGCGTGGCTGTTCTTCTATTTCAGAGCGGAGATGGATCTTATTAATCA 240
DB 181 gtctgagcggtggctgttcttctatttcagagcgagatggatcttataaataca 240
QY 241 GAATATGGCACTCACTGATTTATAGATTGAGCTCATGCAATTAATGAGATTTC 300
DB 241 gaatatggcactcactgatttataagatttgagactcatgcaattatgcaatttca 300
QY 301 GACACAACTGTGAGAGTCAAGATCAAAATTAATACCTGATTCATGAGCAATTAA 360
DB 301 gacacaactgtgagagtcagaatataaataatactgattcagtagagagattaaa 360
QY 361 CAGGCTTTCAAGAGCTGTGCAAAAGAAATTACAACATACGTTGGATCCACACATC 420
DB 361 caggctttcaagagctgtgcaaaagaaattacaacatcgttggatccacacactc 420
QY 421 AGAGCAGGAAGAGCGATGGATGGCTCATGTTAGATTGCGCAGAGGAGCAAGCTT 480
DB 421 agagcaggaagagcgatggatggctcatgtttagatttgccgacagagagagagctt 480
QY 481 GAAGCTCAGCCTTTTGTCTATCTCATCTATTAATGCGCAGCAGATCCCTGTTCCAT 540

DB 481 gaagctcagcctttgtctatctcatctataatgcccacagcatccatctgtcccat 540
QY 541 AAGTAGTCTGCTCTTCTTGTGACATGATCGGGGTTGGGCGCAAGATCCCAATGACT 600
DB 541 aagtagtctgctcttcttgtgacatgactgagagagagagagagagagagagagag 600
QY 601 TTATGCAATGGAAGCAATTAATGATGAGATGAGTGTCTTATACCTGTATGCCAAT 660
DB 601 ttatgcaatggaagcaatataatgagatgagatgagtggtcttataacctgtatgccaat 660
QY 661 TGCTTTGACATCATGAAACTTCAGAGACCTTACCTACAGAGATGCTTCAAGTATG 720
DB 661 tgccttgacatcatgaaacttcagagaccttacctacagagatgcttcaagtatg 720
QY 721 TACCTGCTAAACCCAGCATCAAAATCCCAAGTTCATACCTGTATGGAAGGAGAAC 780
DB 721 tacctgcttaaacccagcatcaaaatcccaagtctcatacctgtatgaagagagagc 780
QY 781 ACCAAGTATTGTCAGGGAATTCTGAATTCATTTTATTCATTAACGTTGGTGGATT 840
DB 781 accaagtattgtcagggaattctgaatttcatttatttccataaacglttgatgatt 840
QY 841 TTTAAGTTACGCTGTGAGAGAGAAATCAGCATGAGGTCACACCCCTCTTACTGGAT 900
DB 841 ttttaagttacgctgtgagagagaaatcagcatgaggtctcacaacctcttactggat 900
QY 901 CCGGATCAGATGCAACATCTTTGGGCTTTTAAAGTTGAGATATGATTA 954
DB 901 cgggatcagatgcaacatctttgggctttttaaagttgagatatagtatga 954

RESULT 2
AAV41372 ID AAV41372 standard; cDNA; 954 BP.
XX AAV41372;
AC 08-OCT-1998 (first entry)
DT XX
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX immune response; inflammatory response; toxic shock; sepsis;
XX RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 1..954 /*tag= a
FT /product= "human RANKL (ligand for RANK)"
W09828424-A2.
PD 02-JUL-1998.
XX 22-DEC-1997; 97WO-US23866.
XX 14-OCT-1997; 97US-0064671.
XX 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX (IMMV) IMMUNEX CORP.
XX Anderson DM, Galibert LJ, Maraskovsky E;
PI WPI: 1998-377655/32.
DR P-PSDB; AAM68293.
XX New isolated receptor activator of necrosis factor-kappa B - useful
PT for, e.g. developing products for regulating an immune or
PT inflammatory response, treating toxic shock or sepsis

are useful for regulating immune response and in screening for inhibitors of these receptors. The cytoplasmic domain of RANK is used in developing assays for inhibitors of signal transduction, e.g. for screening the molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful in ameliorating the negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory reactions and the effects of bone resorption. RANK acts as an anti-apoptotic signal and rescue the cells that express RANK from apoptosis. Soluble forms of the receptor are used in vivo or in vitro based screening tests for agonists or antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B activation, or to inhibit transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast precursors and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is a cDNA encoding human RANK ligand (RANKL) protein.

Sequence 954 BP: 255 A; 239 G; 227 G; 233 T; 0 other;

Query Match 100.0%; Score 954; DB 22; Length 954;
Best Local Similarity 100.0%; Pred. No. 5e-241;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCCGCGCCGACAGACATACACAAAGTACCTGCTGGCTCGAGAGATGGCGCGC 60
DB 1 atgcgccgcgcagagagactaacacaaagtactgctgctcgagagatggcgcgcg 60
QY 61 GGGCCGGAGCCCGCAGAGAGGGCCCTGACAGCCCGCGCGCGCGCGAGACCGC 120
DB 61 gggccggagcccgacagagggccctgacagcccgcgcgcgcgcgagacccag 120
QY 121 CCCCCGCGCGCTCCGCTCCATGTTCTGCGCTCTGCGGCTGGGCTGGCCAGGTT 180
DB 121 cccccgcgcgcctccgcctccatgttcgtgcccctcctggggctgggccaaggtt 180
QY 181 GTCTGACAGCGTGGCCCTGTTCTTATTATTAGAGCGCAGAGATCTTAATGAATATCA 240
DB 181 gtctgacagcgctggccctgttcttattattagagcgagagatcttaataatca 240
QY 241 GAAGATGGACATCATGATTTATAGAAATTTAGAGATCCATGAAGAATTTTCA 300
DB 241 gaagatggacatcatgatttatagaaatttagagatccatgaagaattttcaa 300
QY 301 GACACAACCTCTGGAGATCAGATACAAATTAATACCTGATTCAATGAGAAATTTAA 360
DB 301 gacacaacctctggagatcagatacaaatttaataacctgattcaatgagaatttaa 360
QY 361 CAGGCCCTTTCANAGAGCTGTGCAAAAAGCAATTACAAATATGTTGGATCAAGACATTC 420
DB 361 caggccctttcnaagagctgtgcaaaaagcaattacaataatcgttgatcaagaacatc 420
QY 421 AGAGCGAGAAAGCGATGGTGGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 agagcgagaaagcgatggatgatatgatatgatatgatatgatatgatatgatatgatat 480
QY 481 GAAGCTCAGCCTTTTGCATCTCACTAATTAATGCCAGCAGACATCCATCTGTTCCAT 540
DB 481 gaagctcagccttttgcatctcaactaataatgacacagacatccatctgltccat 540
QY 541 AAAGTAGTCTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
DB 541 aaagttagtctgtcttgt 600

QY 601 TTATGCAATGGAATAATATAGTTAATCAGAGATGCTTTATACCTGTATGCCAATTT 660
DB 601 ttatgcaatggaaataataatagtttaatacagagatgctttatacctgtatgccaattt 660
QY 661 TGGTTTCGACATCATGAAACTTTCAGAGACCTGATCAGAGATATTTCACTAATGCTG 720
DB 661 tggtttcgacatcatgaaacttttcagagacctgatacagagatatttcaactaattgctg 720
QY 721 TAGTCTACTTAAACCCAGATCAAAATCCCAAGTTCATACCTGATGGAAGAGAGACG 780
DB 721 tagtctactttaaacccagatcaaaatcccaagtctcatacctgataaggaaggaagc 780
QY 781 ACCAGATTTGGTCAGAGAAATTCGAATTCATTTTATTCATTAACGTTGGTGAATTT 840
DB 781 accagatttggtcagagaaatttcgaatttcattttatccataaagcttggtgattt 840
QY 841 TTTAAGTTACGGTCTGAGAGAAATTCAGATCAGAGCTCCAAACCCCTCTTACTGAT 900
DB 841 ttttaagttacggcttgagagaaatttcagatcagagctccaaacccctcttactgatt 900
QY 901 CCGGATCAGATGCAACATATTGCGGCTTTAAGTTCGAGTATGATGA 954
DB 901 ccggatcagatgcacatatttgggctttaagttcgaatatagattga 954

RESULT 4

AAD08715 standard; cDNA: 954 BP.

AAD08715;

04-SEP-2001 (first entry)

Human receptor activator of NF- χ B ligand (hRANKL) cDNA.

Human; receptor activator of NF- χ B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response;

chromosome 18q22.1; hRANKL; chromosome 13q14; transmembrane protein; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 1..954

FT /tag= a

FT /product= "Human RANKL protein"

US6242213-B1.

05-JUN-2001.

22-DEC-1997; 97US-0995659.

23-DEC-1996; 96US-0059978.

07-MAR-1997; 97US-0077181.

14-OCT-1997; 97US-0064671.

(IMNV) IMMUNEX CORP.

Anderson DM;

WPI: 2001-407216/43.

P-PSDB; AAE04426.

Claim 2: Column 61-64; 43pp; English.

The present invention relates to receptor activator of NF- χ B (RANK) cDNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane

CC proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening CC for inhibitors of RANK. The present sequence is human RANKL (hRANKL) cDNA.

XX Sequence 954 BP: 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match 100.0%; Score 954; DB 22; Length 954;
Best Local Similarity 100.0%; Pred. No. 5e-241;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ATGCGCGGCGCCAGACAGACTACCAAGTACCTGCGGCGGAGAGATGGCGCGC 60
DB 1 atgcgcgcgccagcgagagacacacacagctcgtcgctcgagagagatggcgcg 60
OY 61 GCGCGCGAGCCCGCAGACAGAGCGCCCGTGCACGCCCGCGCGCTCGCGCAGAC 120
DB 61 gcgcgcgagcccgagacagagcgcccgctgcacgcccgcgcgctcgcgcgacag 120
OY 121 CCGCGCGCGCGCGCGCGTGCATGTTGCGGCGCTCGCGCGCTGGCGCTGGCGCAG 180
DB 121 ccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 180
OY 181 GTCGCGAGCGTGGCGCGCTGTTCTTATTTCAAGCGCAGATGATGATGATGATCA 240
DB 181 gtcgcgagcgctggcgcgctgtcttctatctcagagcgcgagatgcccaatgaa 240
OY 241 GAAGATGCGACATCGCATTTATAGAAATTTGAGACTGCATGAAATGCAATTTTCA 300
DB 241 gaagatgacacacacacacacacacacacacacacacacacacacacacacac 300
OY 301 GACACAACTCTGAGATCAAGTACAAATTAATACGATTCATGATGATGATGATTA 360
DB 301 gacacaaactctgagatcagatcaaaatataacacacacacacacacacacacac 360
OY 361 CAGGCGCTTTCAAGAGCTGTGCAAAAGAAATTACAAATATGCTTGGATTCACAGCAT 420
DB 361 caggcgcttcaagagctgtgcacaaagaaattacaacacacacacacacacacac 420
OY 421 AAGAGAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 aagagagaaagagatgagatgagatgagatgagatgagatgagatgagatgag 480
OY 481 GAAGCTCAGCCCTTTGCTCATCTCTATTAATGCGCAGACATCCATGCTGTTCCAT 540
DB 481 gaagctcagcccttgcctcatctctatataatgcacacacacacacacacacac 540
OY 541 AAGAGTACTGCTGCTCTTGGTACCATGATCGGGTTGGCCAAAGATCTCCAGATGAT 600
DB 541 aagagtactgctgctcttgggtaccatgatcgggttggccaaagatctccagatg 600
OY 601 TTTTACCATGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ttttaccatggaaatataatgattgattgattgattgattgattgattgattgatt 660
OY 661 TGCCTTGCAGATCATGAATTTCAAGAGACCTAGCTACAGATGATCTTCACTAATG 720
DB 661 tgccttgcagatcatgaatttcaagagacctagctacagatgattcttcaactaat 720
OY 721 TACGTCATTAAGACAGATCAAAATTCAGATGATGATGATGATGATGATGATGAT 780
DB 721 tacgtcatataagacagatcaaaatccagattctcatalaccctgataagagag 780
OY 781 ACAAGATTTGTCAGGAAATTTGAATTTCAATTTTATTCATTAAGATGATGATGAT 840
DB 781 acgaagatcttgctcaggaaatctgaatttcaatttcaataaagcttgatgatt 840
OY 841 TTTTAAGTTACGCTGTGAGAGAAATGAGATCGAGTCTTCAACCCCTCTTCTGAT 900
DB 841 ttttaagttacgctgtgagagaaatgagatcgagtcttcaacccctcttctgat 900

```

DB 841 tttaagtacgctgtgagagaaatcagcatcgatgcttccaaacctctctactgat 900
OY 901 CCGATTCAGAGATGACATTAATTTGGGGCTTTTAAAGTTGAGATATGATTTGA 954
DB 901 ccgatctcagatgcacactcttgaggctttaagttcagatagatgattga 954

RESULT 5

ID AAD05904 standard; CDNA: 954 BP.

AC AAD05904;

DT 31-JUL-2001 (first entry)

DE Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA.

DE Human: receptor activator of NF-kappaB; RANK: nuclear factor-kappaB;

KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;

KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopetrotic;

KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;

KW immune system dysfunction; familial expansile osteolysis; FEO;

KW early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14;

OS Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1..954

XX /product= "Human full-length RANKL (receptor activator

XX of NF-kappaB ligand) protein"

XX W0200136637-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000MO-US31459.

XX 17-NOV-1999; 99US-0442029.

XX (IMMUNEX CORP.

XX Anderson DM, Hughes AE;

XX WPI: 2001-329222/34.

XX P-PSDB: AAE01993.

XX New DNA encoding a receptor activator of NF-kappaB polypeptide for the

XX treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -

XX Example 7; Page 75-76; 96pp; English.

The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TNF receptor-associated factors (TRAFs). Triggering of RANK by overexpression or co-expression of the transmembrane bound RANK ligand (RANKL) results in upregulation of NF-kappaB. NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system. Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset Paget's disease of bone (EP). The present sequence is a cDNA encoding full-length human RANKL (hRANKL) protein. The RANKL gene is located in chromosome 13q14.

xx Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
sq

| | | | | |
|-----------------------|-----------------|-------------------|-----------|-------------|
| Query Match | 100.0%; | Score 954; | DB 22; | Length 954; |
| Best Local Similarity | 100.0%; | Pred. NO. 5e-241; | | |
| Matches 954; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0. |

| | | | |
|----|-----|--|-----|
| QY | 1 | ATGCGCGCGGCAGAGAGACTATACCAAGTACCTCGCGCTGCTCGAGAGAAATGGGCGC | 80 |
| Db | 1 | atgcgcgcgccagagagactataccaagtaacctcgctgctcgagagaaatggcgcg | 60 |
| QY | 61 | GGCCCCGGAGCCCCGACAGAGGGCCCCCTGCACGGCCCCGCGCGCTCGCGCCGACAG | 120 |
| Db | 61 | ggccccggagccccgcacagagggccccctgcacggccccgcgcgcgcgcgcgcag | 120 |
| QY | 121 | CCCCCGCGCGCTCCCGGCTCCATGTTCTGCGGCGCTCTGGGGCTGGGCTGGCCAGGTT | 180 |
| Db | 121 | ccccccgcgcctcccgctcccatglttcgtagccctcctcgaggctcgaggtcgcaagt | 180 |
| QY | 181 | GTCTGCAAGCGTGCCTGTCTTCTATTTCACAGCGCAGATGGATTCCTAATGAAATATCA | 240 |
| Db | 181 | gtctcagacgtcgcctgtcttcttactttcacagcgcagatggatctcctaataagaatata | 240 |
| QY | 241 | GAAGATGGCACTACATGCATTTTATAGATTTTGACACTCCAGAAATATGCAGATTTTCAA | 300 |
| Db | 241 | gaagatggcactacatgcattttatagattttgacactccagaataatgcagattttcaa | 300 |
| QY | 301 | GACACAACTCTGAGAGTCAGATACAAAATTATACCTGATTCATGTTGAGCAATTAA | 360 |
| Db | 301 | gacacaaactctgagagtcagatacaaaaaattaatccgattcattgtagagaaatcaa | 360 |
| QY | 361 | CAGGCGCTTCGAAGAGCGTGCAAAAAGAAATTCAACATATCGTTGGATCACAGCAGATC | 420 |
| Db | 361 | caggcgcttcaaggagctgtagcaaaaggaaatcaacatatcgttgtagcaagcaatc | 420 |
| QY | 421 | AGAGCAGAGAAACGATGTGATGGCTCATGCTTAGATCTGGCCAAAGAGCAAGCTT | 480 |
| Db | 421 | agagcagagaaagatggtgtagctgctatgtagatctggccaagagagaaagctt | 480 |
| QY | 481 | GAACCTCAGCGCTTTGGTCATCTCAGATTAATGAAGCCACAGCATCCCATCTGGTCCCAT | 540 |
| Db | 481 | gaacctcagccttctgtctcatctcaactataaagccacagcatcccatctgttcccat | 540 |
| QY | 541 | AAATGAGTGTGTCTCTTGGTACCATGATCGGGGTGGGCCAAGATCTCCAAATGACT | 600 |
| Db | 541 | aaagtggctgtctcctctgttaccatgatacggggttggccaaagatctccaacatgact | 600 |
| QY | 601 | TTTACGCAATGGAACCTAATAGTTAATACAGAGTGGGCTTTATTACCTGATGGCAACATT | 660 |
| Db | 601 | tttagcaatggaaaactaataagtaatacagaatgggcttatttaacctgtatgccaatc | 660 |
| QY | 661 | TGCTTTGCAGATTCATGTAACCTTCAGGAGACTTACTCAGAGTATCTTCAACTAATGGTG | 720 |
| Db | 661 | tgccttgcagactcatgaactctcagagacttagcctacagagatcttcaactaatggtg | 720 |
| QY | 721 | TACGTACTAAACACGATCAATAATCCCAAGTCTCATATACCTCGATGAAGAAGAGAGAGC | 780 |
| Db | 721 | tacgtactaaacaagatcaataatcccaagttctcataccctgataaagagaggaagc | 780 |
| QY | 781 | ACCAAGTATTGGTCAGGAAATTTCGAATTCATTTTATTCATTAACGTTGTGGATTT | 840 |
| Db | 781 | accaagtatattggcagggaaatttcgaattccattttatccataaaagttgtagattt | 840 |
| QY | 841 | TTTAAGTACAGGTCTGAGAGGAAATCGCATCGAGGTCTCCAAACCCCTCCTTACTGGAT | 900 |
| Db | 841 | tttaagttaaggtctcgagaggaatcagatcgaggtctccaaacccctccttactgagt | 900 |
| QY | 901 | CCGATTCAGGATGCACAATCTTTGGGGCTTTAAAGTTGAGATATGATTTGA | 954 |
| Db | 901 | ccgattcaggatgcacaatactttggggctttaaagttcagatatagattga | 954 |

RESULT 6

AAZ99964
ID AAZ99964 standard; DNA; 2271 BP.

AAZ99964;

25-JUL-2000 (first entry)

DNA encoding a human osteoprotegerin ligand (OPGL).

AA osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KM osteoprotegerin receptor; TRAF-6; tumor necrosis factor receptor;
 KM type II transmembrane protein;
 KM tumor necrosis factor receptor; type II transmembrane protein;
 KM osteoclast differentiation; CSF-1; osteoclast activator;
 KM immune response; osteoporosis; bone resorption; ss.

OS Homo sapiens

| | Location/Qualifiers |
|----|---------------------|
| aa | |
| FH | Key |
| FT | 185..1138 |
| | CDS |
| | 433-3 |

WO2000015807-A1.

23-MAR-2000.

13-SEP-1999; 99WO-DK00481.

15-SEP-1998; 98DK-0001164.
02-OCT-1998; 98US-0102896.

(MEBI-) M & E BIOTECH AS.

Halkier T, Haaning J;

WP1; 2000-2/1444/23.
P-PSDB: AAY84417.

In vivo down-regulation

[illegible]

Human C

xx The present sequence encodes a human osteoprotegerin ligand (OPGL).
xx Osteoprotegerin is a secreted member of the tumour necrosis factor
cc receptor family, which blocks osteoclastogenesis in a dose dependent
cc manner. The OPGL protein is synthesised as a type II transmembrane
cc protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
cc is a potent osteoclast differentiation factor when combined with CSF-1.
cc It is not capable of inducing osteoclast differentiation in the absence
cc of CSF-1. OPGL is also an activator of mature osteoclasts. The
cc specification describes a method for the *in vivo* down-regulation of
cc OPGL activity in an animal. The method comprises using at least one OPGL
cc polypeptide or subsequence, and/or at least one OPGL analogue to induce
cc an immune response in the animal. The method and OPGL polypeptide are
cc useful for treating, preventing and ameliorating osteoporosis or other
cc diseases or conditions characterised by excessive bone resorption.

xx Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;
sq

Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;

| | | | | |
|-----------------------|--------------|---------------------|------------|--------------|
| Query Match | 100.0% | Score 954; | DB 21; | Length 2271; |
| Best Local Similarity | 100.0%; | Pred. No. 7.1e-241; | | |
| Matches 954; | Conservative | 0; | Mismatches | 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

OY 1 ATGCGCCGCCGCCAGACAGACTACACCAAGTACTCTGCGTGGCGAGAGATGTGGCCG 60
 Db 185 atgpgccgcgcgcagagagactatacaagaatactctgcf-gtgcgcgagagagatgtggcgcc 244
 OY 61 GGCCTCCGAGCGCTCGCACGAGGGCCCCCTCTGACGCCGCCGCGCGCTGCGCGGCACAG 120
 Db 245 ggcctccgcagccgcgcacagagagagccccctgcacgcgccgcgcgcctctgcgcgcacag 304

| | | | |
|----|------|---|------|
| OY | 121 | CCCCCGCCGCTCCCGCTCCATGTTGCTGGCCCTCCTGGGGCTGGGGCTGGCCAGGTT | 180 |
| OY | 122 | CCCCCGCCGCTCCCGCTCCATGTTGCTGGCCCTCCTGGGGCTGGGGCTGGCCAGGTT | 180 |
| Db | 305 | CCCCCGCCGCTCCCGCTCCATGTTGCTGGCCCTCCTGGGGCTGGGGCTGGCCAGGTT | 364 |
| OY | 181 | GTCCTCAGCGTCGCGCCCTGTTCTTCATTTTCAGACCGGAGATGGATGCTTATACAAATATCA | 240 |
| Db | 365 | gctctgcaagcgctgcgccctgtctctctctatcttcgaagcgagatgagctccaaataaataca | 424 |
| OY | 241 | CAAGATGGCACTCACTGCAATTTATAGAAATTTTGAGACTCCAGTGAATAATGCAGATTTTTCAA | 300 |
| Db | 425 | gaagaatggcaactcactgcattctaaagattcttggactccatgaaatgagaatttccaa | 484 |
| OY | 301 | GACACAACCTCGGAGAGTCAGATATCAAAATTTATACCATTATCTATGTAGAGAAATTTAA | 360 |
| Db | 485 | gacacaacctcggagagcgaaagaaacaaatctaatccattctatctgtagagaaatlaaa | 544 |
| OY | 361 | CAGGCCCTTTCAGAGAGCTGTTCACAAAGAAATTTACAAATATCGTTGGATACAGCAATC | 420 |
| Db | 545 | cagggccttccaagagagctgtgcaaaagaaatcaacaatactgtgtgataccagcaatc | 604 |
| OY | 421 | AGAGCAGAGAAAGCGATGTGTGATGGCTCATGTTAGATCTGGCCAGAGAGCAAGCTT | 480 |
| Db | 605 | agagcagagaaagcgaatggttgaatgctcatgtgtatgactctggcaagagagcaagctt | 664 |
| OY | 481 | GAAGCTCAGCCCTTTTGGCATCTCAGTATTAATATGCAACGCAATCCCATCTGGTCCCAT | 540 |
| Db | 665 | gaagctcagcccttctgtcatctcaaccattaaatgacacgaaatcccatctgttccat | 724 |
| OY | 541 | AAAGTGAAGTCTGCTCTTGGTATCATGATCGGGGTGAGGCCAAGATCTCCAAATGACT | 600 |
| Db | 725 | aaagtgaagctgtctctctgttgaacatgatacgsggttggccaaagttcccaaatgact | 784 |
| OY | 601 | TTTATGCAATGGAAACCTAATATAGTTAATCAGAGATGGCTTTTATTACTGTATGCCAACAT | 660 |
| Db | 785 | cttgcagcaatggaaaacaaatagttaaacaaagatgagcttattatccctgtatgccaact | 844 |
| OY | 661 | TGCTTTGCACATCATGTGAACCTTCAGAGAGACCTAGCTACAGAGATATTCCAAATAGTG | 720 |
| Db | 845 | tgcttctgcacatcaatgaaacttcaagagagccatgactcaagagatattccaactaatgtg | 904 |
| OY | 721 | TACGTCACTAAACACACATCAAAATCCCAAGTTTCATACCCGTGATGAAGAAGAGAGAC | 780 |
| Db | 905 | tacgtcactaaaacaaacatcaaaatcccaagttctcatatccctgtatgaagagagaagc | 964 |
| OY | 781 | ACCAAGATATTGGTCAGGGAATTTCTGAATTCATTTTATTCATTAAGCTGTGGATTT | 840 |
| Db | 965 | accaagatattggttcaggaatcttgaattccatttctatctcaataaagcttggatctt | 1024 |
| OY | 841 | TTTAAAGTTACGTTCTGGAGAGGAATTCAGCATCGAGGTCTCCAAACCCCTCTTACTGAT | 900 |
| Db | 1025 | tttaagttacggtcttggagagaaatcagatctgagtgcttccaaacccctctacttgat | 1088 |
| OY | 901 | CCGAGATCAGATGCACATCTCTTTGGGGCTTTTAAAGTTCGAGATATTAGATTGA | 954 |
| Db | 1085 | cggagatcaggaatgcacaatactcttgggctctttaaagttctcgaaatataagattga | 1138 |

| | |
|----------|--|
| RESULT | 7 |
| AAV70285 | |
| ID | AAV70285 standard; DNA; 2274 bp. |
| XX | |
| AC | AAV70285; |
| XX | |
| DT | 11-FEB-1999 (first entry) |
| XX | |
| DE | Human osteoprotegerin binding protein from the pcdM/hnOpGbp1.linsert. |
| KW | Human; osteoprotegerin binding protein; OPB binding protein; arthritis |
| KW | osteoporosis; osteoclast maturation; bone disease; metastasis; ODA; |
| KW | hypercalcaemia; osteoclast differentiation and activation receptor; |
| KW | Paget's disease; ss. |
| XX | |
| XX | |
| SS | Homo sapiens. |

[illegible]

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Db      425 |||||
Oy      301 GACCAACTGTGAGAGACAGATACAAATTAATACCTGATTGATGAGAGATTAAA
Db      485 gacacaactctggagagcgaagatacaaaaataactgttcatgttaggagattaaa
Oy      361 CAGGCTTTCAAGAGAGCTGTGCAAAAAGATTACAACTATGCTTGGATCAGACATC
Db      545 cagccttcaaggagcgtgcaaaagaaatcacacatacgttgatcacagcacatc
Oy      421 AGAGCAGAGAAAGGATGGTGGATGGCTCATGTTAGATGCGCCAAAGAGAGCAAGCTT
Db      605 agagcagaagaagcgaagtggaagcgaagcgaagcgaagcgaagcgaagcgaagc
Oy      481 GAAGCTCAGCCCTTTGCTCATCTCATATTAATGACACGACATCCATCTGTTCCAT
Db      665 gaagctcagcctttgtccatctcacttaatgacacgacatcccatctgttccat
Oy      541 AAAGTACTGTGCTCTTGGTACCATGATGGGGTTGGCCAGATCTCCAACATGACT
Db      725 aaagtgagctgtccctctgtgacatgatcggggttgycacaagatctcaacatgact
Oy      601 TTTAGCAATGGAAGAACTAATAGTATGAGATGAGTGGCTTTTATTAAGTATGCAACAT
Db      785 tttagcaatgaaaaactaatgataatcagatgagcttttaccgttagcacaact
Oy      661 TGCTTTCAGATCATGAACTTCAGAGAGAGCTAGCTACAGAGATGCTTCACTATGCTG
Db      845 tgccttcgacatcatgaaactcagagagaccagagagagagagagagagagagag
Oy      721 TACGTCACATAAAGCAGATCAAAATCCCAATGCTCATACCTGATGATGAGAGAGAGC
Db      905 taagtcacaaacacagacatcaaacacaaatctcacaacccgtgaagagagagagc
Oy      781 ACCAGTATTTGGTCAAGGAAATTCGAATTCATTTTATTCATTAACGTTGGTGATTT
Db      965 accaagtatgtgcagggagattctgattcatttattcacaacgtgtgtgattt
Oy      841 TTTTAAGTACGGCTGTGAGAGAGAAATCAGATCAGAGTCCACACCCCTTACTGAT
Db      1025 tttaagtaacgtctgagagagaaatcagatcaggtctccaaccccttactgatt
Oy      901 CCGGATCAGAGATGCAACATCTTGGGGCTTTAAAGTTCGAGATATGATTTGA
Db      1085 ccgagacagagatgacaacactttg99gctttaaagttcgagataagattga

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XX      02-DEC-1997; 97JP-0332241.
PR      15-APR-1997; 97JP-0097808.
PR      09-JUN-1997; 97JP-0151434.
PR      12-AUG-1997; 97JP-0217897.
PR      21-AUG-1997; 97JP-0224803.
XX      (SNOW ) SNOW BRAND MILK PROD CO LTD.
PA      Goto M, Hiasashio K, Kinoshaki M, Kobayashi F, Morinaga T;
PI      Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI      Washida N, Yamaguchi K, Yano K, Yasuda H;
XX      WPI: 1998-594563/50.
DR      P-PSDB; AAM83018.
XX      Protein binding to osteoclastogenesis inhibitory factor - useful
PT      for, e.g. treatment and investigation of disorders of bone and
PT      calcium metabolism
XX      Claim 38; Page 115; 151pp; Japanese.
PS      The present sequence encodes an osteoclastogenesis inhibitory factor
CC      (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC      separation and maturation of osteoclasts in the presence of bone
CC      absorption factors such as calcitriol or parathyroid hormone (PTH).
CC      OBM is isolated from stroma cells cultured in the presence of a bone
CC      absorption factor by separation and solubilisation of membrane proteins
CC      then affinity chromatography using OCIF. It exists in a full-sequence
CC      form and a solubilised form (SOBM) which is a shorter chain. OBM may be
CC      used for screening potential inhibitors and modifiers of its function.
CC      activity, and screening for receptors to OBM which mediate its function.
CC      These substances can then be used in the treatment of disorders of bone
CC      function and calcium metabolism. The antibodies can be used for assay
CC      of the protein, for investigative and diagnostic purposes, and as
CC      components of drugs.
XX      Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
SQ

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Query Match 99.7%; Score 950.8; DB 19; Length 954;
Best Local Similarity 99.8%; Pred. No. 3; 5e-240;
Matches 952; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Oy      1 ATGCGCGCGCGCAGCAGAGACTACACCAAGTACCTGCTGCTCGAGAGATGGCGGC
Db      1 atgcgcgcgcgagagactaacacaaagtaacctgctgctcgagagatggcggc
Oy      61 GGCGCCGAGGCCCGCAGAGAGGGCCCTCGACGCGCCGCGCGCGCGCAGACAG
Db      61 ggcgcccagagcccgcagagagcgccccctgcagcgcccgccgctgcgcgcacag
Oy      121 CCCCGCGCGCGCTCCGCTCCATGTTCTGCGCCCTCTGCGGGCTGCGGCGAGGTT
Db      121 cccctgcgcgctcccgctccatgttctgtgcccctcccggggcttggggccaggtt
Oy      181 GTCCTCAGCGTGGCCCTGTTCTTATTTACAGCGCGAGATGATCTTAATGAATATCA
Db      181 gtcctcagcgctggccctgttcttctatctcagagcgagatgataatgaatca
Oy      241 GAAGATGGACGACACTGCAATTTATGAAATTTGACACTCCATGAAATGCAAGATTTC
Db      241 gaagatggacactgcaactttagaatttgaagatccatgaaatgaagatattcaa
Oy      301 GACCAACTGTGAGAGATCAAGATCAAAATTAATACCTGATTGATGAGGAATTAAA
Db      301 gacacaactctggagagtgtaagatacaaaaataactgttcatgttaggagattaaa
Oy      361 CAGGCTTTCAAGAGAGCTGTGCAAAAAGATTACAACTATGCTTGGATCAGACATC
Db      361 cagccttcaaggagcgtgcaaaagaaatcacacatacgttgatcacagcacatc
Oy      421 AGAGCAGAGAAAGGATGGTGGATGGCTCATGTTAGATGCGCCAAAGAGAGCAAGCTT

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|||||
Db 601 ttattccataaacgttggatgttttaagtacggtcctgaggaatacagc 660
QY 874 GAGGCTCCAAACCCCTCTACTGATCGATCAGATGCAACATACCTTTGGGCTTTT 933
Db 661 gaggctcccaaccctcttactgataccgatacagatgcacactacttgggctt 720
QY 934 AAAGTTGAGATATAGATTGA 954
Db 721 aaagtcgagatatagtga 741

RESULT 10
AA80223
ID AA80223 standard; cDNA; 1823 BP.
AC AA80223;
XX 17-AUG-1999 (first entry)
XX Human TRANCE encoding cDNA.
XX
XX TRANCE: tumour necrosis factor superfamily; signal transduction; TNF;
XX TNF-related activation induced cytokine; immune response; cancer;
XX autoimmune disease; HIV; hypersensitivity; allergen; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..738
XX FT /*tag= a
XX PN W0929865-A2.
XX
XX 17-JUN-1999.
XX
XX 14-DEC-1998: 98WO-US26486.
XX
XX 11-DEC-1998: 98US-0989479.
XX 12-DEC-1997: 97US-0989479.
XX 03-MAR-1998: 98US-0034099.
XX
XX (UYRO ) UNIV ROCKEFELLER.
XX
XX Choi Y, Josien R, Steinman R, Won B;
XX WPI: 1999-385609/32.
XX P-PSDB; AAY17873.
XX
XX TNF like proteins for treating autoimmunity and cancer
XX
XX Claim 1: Fig 1; 164pp; English.
XX
XX The present sequence encodes human TNF-related activation induced
XX cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX variants, fragments, derivatives or analogues may be used as modulators
XX of immune response in a mammal comprising: antisense sequences to
XX TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX Agonists and antagonists of TRANCE, can be used to modulate immune
XX response by increasing or decreasing the life span of mature dendritic
XX cells and increasing or decreasing T cell activation. These techniques
XX are especially useful for treating immune system related conditions such
XX as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX The TRANCE polypeptides can be used to increase the viability of
XX dendritic cells in vivo or in vitro, especially when used in conjunction
XX with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CD40L or TNF-alpha).
XX
XX Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;

Query Match 76.9%; Score 733.2; DB 20; Length 1823;
Best Local Similarity 99.6%; Pred. No. 8e-183;
```

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Matches 735; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 217 CAGATGATCCTTAATACAAATATCAGAAATGGCACTCCAGCAATTATAGAAATTTTGA 276
Db 1 cagatgatacctaataataatcagaatgacatgcacatcactatcagaatlttgaga 60
QY 277 CTCGATGAAATGCAGATTTTTCAGACACAACCTCGAGAGTCAAGATACAAAATTAATA 336
Db 61 ctccatgaaatgacagatlttccaagacacacctctgagatcagaatataata 120
QY 337 CCTGATTCATGTAGAGAAATTAACAGGCTTTTAAAGAGCTGTCGCAAAAGAAATTCAA 396
Db 121 cctgattcatgtagagaaatlaaacagccttlaaagagactgycaaagaaatlaaa 180
QY 397 CATATCGTTGATCATACAGACATCATCAGACAGAGAAAGATGTGATGGCTCATGTGTTA 456
Db 181 catatcgttgcacacacacacacacacacacacacacacacacacacacacacacac 240
QY 457 GATCTGGCCAAAGAGAGCAAGCTTGAAGCTCAGGCTTTTGCTCATCTATTAAATGCC 516
Db 241 gatctggccaaagagagagagagagagagagagagagagagagagagagagagag 300
QY 517 ACCGACATCCCATCTGCTTCCCATTAAGTGAAGTCTGCTCTTGTGACATGCGGGGT 576
Db 301 accgacatcccatctggtcccataaagtgaagctgctccttgcacacacacacacac 360
QY 577 TGGGCCAAGATCCCAATGACCTTTAGCAATGAGAAATTAATAGTTAATCAGATGGC 636
Db 361 tggggtaagatctccaacatgactttagcaatggaataactaatagtaacacagatggc 420
QY 637 TTTTATTAACCTGTATGCCAACATTTGCTTGCATCATGAATCTTACGAGACCTAGCT 696
Db 421 ttattatcctgtatgccaaactgttctgcacatcagaaactcagagacttagct 480
QY 697 ACAGAGATATCTTCACACTAATAGTGTAGCTCACTAAACAGACATCAAAATCCAAATGCT 756
Db 481 acagagatattcaactaatgtgtcagtcactaaacacacacacacacacacacac 540
QY 757 CATACCTGATGAAGAGAGAGACCAAGTATTTGGTCAGGGAATTCGAATTCATTTT 816
Db 541 cataccctgataaagagagagagagagagagagagagagagagagagagagagag 600
QY 817 TATTCATTAACGTTGGTGGATTTTAAAGTTAGCGTCTGGAGAGGAATACGATCGAG 876
Db 601 tattccataaacgttggatgttttlaagtlacggtctgagaggaatacagacatcgag 660
QY 877 GGTCCCAACCCCTTACTGATCGGATCGATGCAACATACCTTTGGGCTTTTAAA 936
Db 661 gtcccaaccccttactgataccgatacagatgcagatacactacttgggctttaa 720
QY 937 GTTCGAGATATAGATTGA 954
Db 721 gtccgagatatagtga 738

RESULT 11
AAF86481
ID AAF86481 standard; cDNA; 957 BP.
XX
XX AAF86481;
XX
XX 29-JUN-2001 (first entry)
XX
XX Rat osteoclast differentiation factor. ODF, coding sequence.
XX
XX Rat: osteoclast formation inducer; vaccine; gene therapy;
XX Osteoclast Differentiation Factor; bone; ss.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..957
XX FT /*tag= a
```



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OY 1 ATGCGCGCGCCAGACAGACTACCAAGTACCTGCGTGGCTGGAGAGAGATGGCGGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 60
OY 61 GGGCCCGAGAGCGCCGACAGAGGCGCCCTGCACGCCCGCCG---GGCGGCTGGCGCGCAC 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ggcgcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 120
OY 118 CAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 cgcgacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 180
OY 178 GTTGTCTGCAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 gtagtcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
OY 238 TCAGAGATGGCACTCACTGATTTATAGAAATTTGAGACTCCATGAAATGCAAGATTTT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 tcagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
OY 298 CAGACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATTCATGAGAGAAATT 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 cagagacgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 354
OY 358 AACACAGCGCTTTCAAGAGCTGTGCCAAAGAGATTTACACATATCTGTGATCACAGCAC 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 aacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 414
OY 418 ATCAGACAGAGAAAGGATGGATGGCGATGGTATGATGCGCAAGAGAGAGAGAG 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 ttcacagagagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 474
OY 478 CTTCAGACTCAGCGCTTTGCTCATCTCATATTAATGCGACGACGACATCCATCTGCTTCC 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 ccgagagcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 534
OY 538 CATTAAGTCACTCTGCTCTCTGTTACCATGATGCGGGTGGCCCAAGATCTCCACATG 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 cataaagtcacctcgtcctcctcgtcagcagcagcagcagcagcagcagcagcagcagc 594
OY 598 ACTTTTGCATGGAATGAACTAAATGAGATGAGTCTTTTACCTGATGCGCAC 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 acgtlaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagc 654
OY 658 ATTTGCTTGCATGATGAATTTACAGAGACCTAGCTACAGATGATCTTCAACTAATG 717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 attgccttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 714
OY 718 GTGTACGTCACTAAACCCAGCATCAAAATCCCAAGTTCTCATACCTGTGATGAAGAGA 777
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 715 gtagtctcgtlaaaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 774
OY 778 AGCACCAAGTATTTGATGAGGAATTCGATTTTATTCATTAACGTTGGTGA 837
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 775 agcagcaaaacatgagcagcaatcagcaatcagcaatcagcaatcagcaatcagcaatcagc 834
OY 838 TTTTATGATTCAGCTGTGAGAGAAATCAGATCAGATCTTCCAAACCCCTCTACTG 897
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 835 ttttcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 894
OY 898 GATCCGATCAGATGCAACATCTTTGGGGCTTTAAAGTTGAGATATAGATTGA 954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 895 gatccgagtcagagtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 951

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RESULT 14

AAZ99965 standard; DNA: 951 BP.

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XX AAZ99965:
XX
XX 25-JUL-2000 (first entry)
XX

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DE DNA encoding a murine osteoprotegerin ligand (OPGL).
XX
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..951
FT
FT /tag= a
FT /product= "osteoprotegerin ligand"
XX
Db W0200015807-A1.
XX
Db 23-MAR-2000.
XX
Db 13-SEP-1999; 99WO-DK00481.
XX
Db 15-SEP-1998; 98DK-0001164.
XX
Db 02-OCT-1998; 98US-0102896.
XX
Db (MEBI-) M & E BIOTECH AS.
XX
Db Halkier T, Haaning J;
XX
Db WPI: 2000-271444/23.
XX
Db P-PSDB; AAY84418.
XX
Pt In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
Pt to treat, prevent and ameliorate osteoporosis -
XX
Ps Disclosure; Page 79-81; 110pp; English.
XX
Cc The present sequence encodes a murine osteoprotegerin ligand (OPGL).
Cc Osteoprotegerin is a secreted member of the tumour necrosis factor
Cc receptor family, which blocks osteoclastogenesis in a dose dependent
Cc manner. The OPGL protein is synthesised as a type II transmembrane
Cc protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
Cc is a potent osteoclast differentiation factor when combined with CSF-1.
Cc It is not capable of inducing osteoclast differentiation in the absence
Cc of CSF-1. OPGL is also an activator of mature osteoclasts. The
Cc specification describes a method for the in vivo down-regulation of
Cc OPGL activity in an animal. The method comprises using at least one OPGL
Cc polypeptide or subsequence, and/or at least one OPGL analogue to induce
Cc an immune response in the animal. The method and OPGL polypeptide are
Cc useful for treating, preventing and ameliorating osteoporosis or other
Cc diseases or conditions characterised by excessive bone resorption.
XX
S0 Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other:

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Query Match 69.8%; Score 666.2; DB 21; Length 951;
Best Local Similarity 82.5%; Pred. No. 2.0e-165;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

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OY 1 ATGCGCGCGCCAGACAGACTACCAAGTACCTGCGTGGCTGGAGAGATGGCGGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 60
OY 61 GGGCCCGAGAGCGCCGACAGAGGCGCCCTGCACGCCCGCCG---GGCGGCTGGCGCGCAC 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ggcgcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 120
OY 118 CAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 cgcgacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 180
OY 178 GTTGTCTGCAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 gtagtcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240

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OY 238 TCAGAGATGGCACTCACTGATTTATAGAAATTTTGAGACTCCATGAAATGTCAGATT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 tcagaagaacagactcactgcttltatagaatcctcgactccatgaaagcggtt 300
OY 298 CAAGACAACTCTGGAGAGTCAAGATACAAATTAATACCTGATTCATGTAGAGAA 357
    || || || || || || || || || || || || || || || || || || || || ||
Db 301 cagactcagactcgtgagagtgaaagac-----actactgctcctcgtgagagtg 354
OY 358 AAAAGGCTTTCAAGAGCTGTGCAAAAGAAATTAACAACTATCGTTGATTCACAGAC 417
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Db 355 aaacaagccttcaggggcccgtgcgaagaagactgcaacatctgtgggcccacagcgc 414
OY 418 ATCAGACAGAGAAAGGATGGTGGTCAATGCTATGCTGAGCCAAAGAGAGCAAG 477
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Db 415 ttctcagagagctcagctatgataiggaagctcagtggttggtggcccaagcggaag 474
OY 478 CTGGAAGCTGACCTTTTGTCTCATCTCATTAATATGCGACGACATCCCATCTGCTTC 537
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Db 475 cctgagggcccgcatctgacacctcacatcaatgctgcagacatcccatcggttcc 534
OY 538 CATAAAGTACTCTGCTCTCTTGTACCATGATGGGGTTGGGCAANATCTCCAAACATG 597
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Db 535 cataaagctactcgtccctcttgtaaccaagtcgaagcgtggccaaatctctaaacatg 594
OY 598 ACTTTAGCAATGGAACCTAATAGTATGAGATGGCTTTTATTAACCTGATGCGCAAC 657
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Db 655 attgcttcgcgcatcaagaacacgcggaagcgtlaactaagaactactctcaactg 714
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OY 898 GATCCGGATCGAGTGCACATACTTGGGCTTTTAAAGTTCGAGATATGATTGA 954
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RESULT 15

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AAZ49024
ID AAZ49024 standard; DNA; 951 BP.
XX
AC AAZ49024:
XX
DT 31-MAR-2000 (first entry)
XX
DE osteoclast formation promoting factor coding sequence.
XX
KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;
KM bone metabolic disease; osteoporosis; therapy; ss.
XX
OS Mus sp.
XX
PN JF11332581-A.
XX
PD 07-DEC-1999.
XX
PF 20-OCT-1998; 98JP-0316973.
XX
PR 24-MAR-1998; 98JP-0076232.
XX
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
```

```
PA (SANY ) SANKYO CO LTD.
XX
DR WPI; 2000-091362/08.
XX
PT A new protein, a DNA and its application -
XX
PS Example 1; Page 13; 18pp; Japanese.
XX
CC This sequence encodes the osteoclast formation promoting factor (OBM).
CC The invention relates to an OBM binding protein (OBM-BP). The protein is
CC useful as a preventive and/or treating agent for bone metabolic diseases
CC such as osteoporosis. Substances which inhibit the binding of OBM to
CC OBM-BP can be used as biochemical reagents.
XX
SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;
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Query Match 69.8%; Score 666.2; DB 21; Length 951;
Best Local Similarity 82.5%; Pred. No. 2.6e-165;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

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Db 1 atgcgcggcgccagcgagactacgcaagtaactcgtgcagctcgagagatgagagcagc 60
OY 61 GGCCCGGAGCCCGCACAGAGGGCCCTCGCACGCCCGC---CGCGCCTGCGCGCCGAC 117
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Db 61 ggcgcggcgcccgcaacaagaggtcgcgtgcaccccgscgtcttgcaacgcgcgcgcgcg 120
OY 118 CAGCCCGCCGCGCGCTCCGCTCCATGTTGCGGCCCTCTCGGGCTGGGGCTGGGCCAG 177
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Db 121 ccgcaccccgcgctcccgctccatgtctcgtgcccctctggggcgtgagactggccag 180
OY 178 GTGTCGTCAGCGTCGCGCCCTGTTCTTATTTTCAGAGCGAGATGAGATCTTAATAGAA 237
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OY 238 TCAGAGATGGCACTCACTGATTTATAGAAATTTTGAGACTCCATGAAATGAGATT 297
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OY 538 CATAAAGTACTCTGCTCTCTTGTACCATGATGGGGTTGGGCAANATCTCCAAACATG 597
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Db 535 cataaagctactcgtccctcttgtaaccaagtcgaagcgtggccaaatctctaaacatg 594
OY 598 ACTTTAGCAATGGAACCTAATAGTATGAGATGGCTTTTATTAACCTGATGCGCAAC 657
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Db 595 acgttaagcaacggaataactaaggttaaccaagtgctctatctactctgtaagccaac 654
OY 658 ATTTGCTTTGCACATCATGAACCTTCAGAGACCTAGCTACAGAGTATCTTCAACTATG 717
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Db 655 attgcttcgcgcatcaagaacacgcggaagcgtlaactaagaactactctcaactg 714
OY 718 GTGACGTCATTAACACGATCAAAATCCCAAGTCTTACCCCTATGAAAAGAGAGA 777
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Db 715 gtcgatacgcgttaaaacagcatcaaaatcccaagttctcaataactgtaaaaagaggg 774
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OY 838 TTTTAAAGTTACGTCGTGAGAGAAATCAGATCGAGTCTCCAAACCCCTCTACTG 897
Db 835 ttctcaagctccgagctggtgagaatlaagatcagggtgccaaaccttccctgctg 894
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Search completed: July 8, 2002, 21:43:51
Job time: 6085 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 20:04:31 ; Search time 96.15 Seconds
(without alignments)
2437.175 Million cell updates/sec

Title: US-09-865-363-12
Perfect score: 954
Sequence: 1 ATCGCCGCCGCCAGCAGAGA.....AAGTTCAGATATGATTGA 954

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq: *
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5: /cgn2_6/ptodata/2/1na/PCMus.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
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| 1 | 954 | 100.0 | 954 | 3 | US-08-996-139-12 |
| 2 | 954 | 100.0 | 954 | 4 | US-08-995-659-12 |
| 3 | 954 | 100.0 | 954 | 4 | US-09-215-649A-12 |
| 4 | 954 | 100.0 | 2271 | 4 | US-09-052-521C-3 |
| 5 | 666.2 | 69.8 | 2191 | 4 | US-08-989-362-1 |
| 6 | 666.2 | 69.8 | 2295 | 2 | US-08-842-842-6 |
| 7 | 666.2 | 69.8 | 2295 | 4 | US-09-052-521C-1 |
| 8 | 615 | 64.5 | 1630 | 3 | US-08-996-139-10 |
| 9 | 615 | 64.5 | 1630 | 4 | US-08-995-659-10 |
| 10 | 615 | 64.5 | 1630 | 4 | US-09-215-649A-10 |
| 11 | 69.4 | 7.3 | 759 | 4 | US-09-320-424-12 |
| 12 | 69.4 | 7.3 | 768 | 4 | US-09-320-424-10 |
| 13 | 69.4 | 7.3 | 1042 | 3 | US-08-584-031-2 |
| 14 | 69.4 | 7.3 | 1042 | 3 | US-08-780-486-2 |
| 15 | 69.4 | 7.3 | 1521 | 1 | US-08-670-354-3 |
| 16 | 69.4 | 7.3 | 1521 | 4 | US-09-320-424-3 |
| 17 | 69.4 | 7.3 | 1521 | 5 | PCT-US96-10895-3 |
| 18 | 69.4 | 7.3 | 1751 | 1 | US-08-670-354-1 |
| 19 | 69.4 | 7.3 | 1751 | 4 | US-09-320-424-1 |
| 20 | 69.4 | 7.3 | 1751 | 5 | PCT-US96-10895-1 |
| 21 | 69.4 | 7.3 | 1769 | 4 | US-09-333-593A-5 |
| 22 | 69.4 | 7.3 | 1769 | 4 | US-09-505-250-1 |
| 23 | 57.6 | 6.0 | 1366 | 1 | US-08-670-354-5 |
| 24 | 57.6 | 6.0 | 1366 | 4 | US-09-320-424-5 |
| 25 | 57.6 | 6.0 | 1366 | 5 | PCT-US96-10895-5 |
| 26 | 41.8 | 4.4 | 15331 | 3 | US-09-128-155-16 |
| 27 | 41.4 | 4.3 | 1777 | 1 | US-08-173-508-5 |

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| 28 | 41.4 | 4.3 | 1777 | 2 | US-08-265-310-5 | Sequence 5, Appl11 |
| 29 | 41.4 | 4.3 | 1777 | 2 | US-08-951-742-5 | Sequence 5, Appl11 |
| 30 | 40.6 | 4.3 | 44377 | 2 | US-08-804-227C-7 | Sequence 7, Appl11 |
| 31 | 40.6 | 4.3 | 44377 | 2 | US-08-804-198-1 | Sequence 1, Appl11 |
| 32 | 40 | 4.2 | 2000 | 4 | US-08-426-509A-1 | Sequence 1, Appl11 |
| C 33 | 40 | 4.2 | 2000 | 5 | PCT-US95-05008-1 | Sequence 1, Appl11 |
| C 34 | 40 | 4.2 | 30001 | 1 | US-08-125-468-1 | Sequence 1, Appl11 |
| C 35 | 40 | 4.2 | 30001 | 2 | US-08-474-933-1 | Sequence 1, Appl11 |
| 36 | 39.4 | 4.1 | 4451 | 3 | US-08-717-284-42 | Sequence 42, Appl11 |
| 37 | 39.2 | 4.1 | 5474 | 4 | US-09-040-738-1 | Sequence 1, Appl11 |
| 38 | 39.2 | 4.1 | 5474 | 4 | US-08-652-426A-1 | Sequence 1, Appl11 |
| 39 | 39 | 4.1 | 1853 | 4 | US-08-952-061-1 | Sequence 1, Appl11 |
| 40 | 38.8 | 4.1 | 1485 | 1 | US-08-471-601-23 | Sequence 23, Appl11 |
| 41 | 38.8 | 4.1 | 1485 | 1 | US-08-474-556-23 | Sequence 23, Appl11 |
| 42 | 38.8 | 4.1 | 1485 | 1 | US-08-479-382-23 | Sequence 23, Appl11 |
| 43 | 38.8 | 4.1 | 1485 | 1 | US-08-470-354-23 | Sequence 23, Appl11 |
| 44 | 38.8 | 4.1 | 1485 | 1 | US-08-479-383-23 | Sequence 23, Appl11 |
| 45 | 38.8 | 4.1 | 1485 | 2 | US-08-479-041-23 | Sequence 23, Appl11 |

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

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? ANTI-SENSE: NO
? ORIGINAL_SOURCE:
? ORGANISM: Homo sapiens
? IMMEDIATE_SOURCE:
? LIBRARY:
? CLONE: huRANKL (full length)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..951
? US-08-996-139-12
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| Query Match 954: 100.0%; Score 954; DB 3; Length 954; | |
| Best Local Similarity 100.0%; Pred. No. 2,5e-251; | |
| Matches | 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| OY | 1 ATGCGCGCGCGCAGAGACTACCAAGTACTGCGTCCGAGGAGATGGCGGC 60 |
| Db | 1 ATGCGCGCGCGCAGAGAGACTACCAAGTACTGCGTCCGAGGAGATGGCGGC 60 |
| OY | 61 GGGCGCGGAGCGCGCAGAGAGGGCCCCGCGACGCGCGCGCGCTCGCGCGACG 120 |
| Db | 61 GGGCGCGGAGCGCGCAGAGAGGGCCCCGCGACGCGCGCGCGCTCGCGCGACG 120 |
| OY | 121 CCCCCCGCGCGCTCCCGCTCCATGTTTCGTGGCCCTCTGGGGCTGGGGCCAGGTT 180 |
| Db | 121 CCCCCCGCGCGCTCCCGCTCCATGTTTCGTGGCCCTCTGGGGCTGGGGCCAGGTT 180 |
| OY | 181 GTCCTCAGCGTCGCCCTGTCTTCTTATTCAGAGCGCAATGGATCCTATAGAAATATCA 240 |
| Db | 181 GTCCTCAGCGTCGCCCTGTCTTCTTATTCAGAGCGCAATGGATCCTATAGAAATATCA 240 |
| OY | 241 GAAGATGGCAGCTACCTGCATTTATAGAAATTTGAGACTCCATGAAATSCAGATTTTCAA 300 |
| Db | 241 GAAGATGGCAGCTACCTGCATTTATAGAAATTTGAGACTCCATGAAATSCAGATTTTCAA 300 |
| OY | 301 GACACAACTCTGAGAGATTAAGATACAAAATTAATACCTGATTCAATGTAGGAGAAATTAA 360 |
| Db | 301 GACACAACTCTGAGAGATTAAGATACAAAATTAATACCTGATTCAATGTAGGAGAAATTAA 360 |
| OY | 361 CAGGCTTTCAAGAGAGCTGTGCAAAAAGAAATTAACAATATCGTTGGATCACAGCAATC 420 |
| Db | 361 CAGGCTTTCAAGAGAGCTGTGCAAAAAGAAATTAACAATATCGTTGGATCACAGCAATC 420 |
| OY | 421 AGAGCAGAGAAAGCGATGGTGGATGGCTCATGTAGATCTGGCCAAAGAGCAAGCTT 480 |
| Db | 421 AGAGCAGAGAAAGCGATGGTGGATGGCTCATGTAGATCTGGCCAAAGAGCAAGCTT 480 |
| OY | 481 GAAGCTCAGCCCTTTGGCTCATCATCTAATTAATGCCACGACATCCCATCGGTTCCCAT 540 |
| Db | 481 GAAGCTCAGCCCTTTGGCTCATCATCTAATTAATGCCACGACATCCCATCGGTTCCCAT 540 |
| OY | 541 AAGTGAGTCTGTCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCAACTAGCT 600 |
| Db | 541 AAGTGAGTCTGTCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCAACTAGCT 600 |
| OY | 601 TTTAGCAATGGAANAATATAGTTATTCAGAGAGCGCTTTATTAACCTGATGCCAATTT 660 |
| Db | 601 TTTAGCAATGGAANAATATAGTTATTCAGAGAGCGCTTTATTAACCTGATGCCAATTT 660 |
| OY | 661 TGCCTTGCAGATCATGAAGATTCAGAGAGACTAGCTACAGAGATCTTCAACTAATGGTG 720 |
| Db | 661 TGCCTTGCAGATCATGAAGATTCAGAGAGACTAGCTACAGAGATCTTCAACTAATGGTG 720 |
| OY | 721 TACGTCACATAAAACAGCATCAAAATCCCAAGTTCATACCTGATGAAGAGAGAGAGC 780 |
| Db | 721 TACGTCACATAAAACAGCATCAAAATCCCAAGTTCATACCTGATGAAGAGAGAGAGC 780 |
| OY | 781 ACCAAGTATTTGGCAGAGGAATTCGAATTCATTTTATTCATAAAGCGTTGGTGATTT 840 |
| Db | 781 ACCAAGTATTTGGCAGAGGAATTCGAATTCATTTTATTCATAAAGCGTTGGTGATTT 840 |
| OY | 841 TTTTAAGTACGGCTCTGGAGAGGAATTCAGATCAGAGCTCCACCCCTCTTACTGAGAT 900 |

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Db 901 CCGGATTCAGGATGCACATACTTTGGGGCTTTTAAAGTCGAGTATATAGATTGA 954

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RESULT 2
US-08-995-659-12
; Sequence 12, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 954 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: hURANKL (full length)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
US-08-995-659-12

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| Query Match | 100.0% | Score 954 | DB 251 | Length 954 |
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| Matches 954 | Conservative | 0 | Mismatches | 0 |
| | | | Indels | 0 |
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| DB | 1 | ATGCGCGCGCGCCGACAGAGACTACACCAAGTACTCTCGTGGCTCGGAGAGATGGCGGC | 60 | |
| OY | 61 | GGCGCCGGAGCCCCCGACAGAGGGCCCCCTGACAGCCCCCGCGCTCGCGCCAGCAG | 120 | |
| DB | 61 | GGCGCCGGAGCCCCCGACAGAGGGCCCCCTGACAGCCCCCGCGCTCGCGCCAGCAG | 120 | |
| OY | 121 | CCCCCGCGCGCCCTCCGCTCCATGTTGCGGGCCCTCTGGGGCTGGGGCCAGGTT | 180 | |
| DB | 121 | CCCCCGCGCGCCCTCCGCTCCATGTTGCGGGCCCTCTGGGGCTGGGGCCAGGTT | 180 | |
| OY | 181 | GTCGCGAGCGTCGCCCTGTTCTTCTATTTTCAGAGCGCAGATGGATCCTAATGAATATCA | 240 | |
| DB | 181 | GTCGCGAGCGTCGCCCTGTTCTTCTATTTTCAGAGCGCAGATGGATCCTAATGAATATCA | 240 | |
| OY | 241 | GAAGATGGGACATCAGTCATATGAATTTTGAAGCTCCATGAAATGCAATTTTCAA | 300 | |
| DB | 241 | GAAGATGGGACATCAGTCATATGAATTTTGAAGCTCCATGAAATGCAATTTTCAA | 300 | |
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| DB | 301 | GACACAATCTGGAGAGTCAGATACAAATTAATACCTGATTCATGTAGAGAAATTAA | 360 | |
| OY | 361 | CAGGCTTTCAAGAGAGCTGTGCAGAAAGAAATTACACATATCTGGTGAACAGCACATC | 420 | |
| DB | 361 | CAGGCTTTCAAGAGAGCTGTGCAGAAAGAAATTACACATATCTGGTGAACAGCACATC | 420 | |
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| DB | 421 | ACAGCAGAGAAAGCATGGTGGATGGCTCATGTTAGATCTGGCCAAAGAGAGCAAGCT | 480 | |
| OY | 481 | GAAAGCTCAGCCTTTTGGCTCATCTCACTATTTAATGCGCACGACATCCATCTGGTCCCAT | 540 | |
| DB | 481 | GAAAGCTCAGCCTTTTGGCTCATCTCACTATTTAATGCGCACGACATCCATCTGGTCCCAT | 540 | |
| OY | 541 | AAAGTGAAGCTCTGCTCTGGTGAACATGATGGGGGTGGGCCAAGATGCTCCAACTGAGCT | 600 | |
| DB | 541 | AAAGTGAAGCTCTGCTCTGGTGAACATGATGGGGGTGGGCCAAGATGCTCCAACTGAGCT | 600 | |
| OY | 601 | TTTACCAATGAGAAACTAATAGTAATCAGATGGCTTTTATTTACCTGTATGCCAATTT | 660 | |
| DB | 601 | TTTACCAATGAGAAACTAATAGTAATCAGATGGCTTTTATTTACCTGTATGCCAATTT | 660 | |
| OY | 661 | TGCTTTCGACATCAGAACTTCAGAGAACCTCAGACCTAGCTACAGAGTATCTTCAACTAATGCTG | 720 | |
| DB | 661 | TGCTTTCGACATCAGAACTTCAGAGAACCTCAGACCTAGCTACAGAGTATCTTCAACTAATGCTG | 720 | |
| OY | 721 | TACGTCACATAAACCCAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAAGGAGGAGC | 780 | |
| DB | 721 | TACGTCACATAAACCCAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAAGGAGGAGC | 780 | |
| OY | 781 | ACCAAGTATGTGTCAGGGAATTTGCAATTTTATTTCCATTAACGTTGGTGAGATT | 840 | |
| DB | 781 | ACCAAGTATGTGTCAGGGAATTTGCAATTTTATTTCCATTAACGTTGGTGAGATT | 840 | |
| OY | 841 | TTTAAGTACAGGTGCGAGAGAAATCGCATCGAGGCTCCAAACCCCTCTACTGAGAT | 900 | |
| DB | 841 | TTTAAGTACAGGTGCGAGAGAAATCGCATCGAGGCTCCAAACCCCTCTACTGAGAT | 900 | |
| OY | 901 | CCGAGTCAAGATGCAACATACTTTGGGGCTTTTAAAGTTTCAGATATATGATTGA | 954 | |
| DB | 901 | CCGAGTCAAGATGCAACATACTTTGGGGCTTTTAAAGTTTCAGATATATGATTGA | 954 | |

```

1 GENERAL INFORMATION:
2 APPLICANT: Anderson, Dirk M.
3 Galibert, Laurent
4 Maraskovsky, Eugene
5 TITLE OF INVENTION: Receptor Activator of NF-kappaB
6 NUMBER OF SEQUENCES: 19
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Immunex Corporation, Law Department
9 STREET: 51 University Street
10 CITY: Seattle
11 STATE: WA
12 COUNTRY: USA
13 ZIP: 98101
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 OPERATING SYSTEM: Apple Operating System 7.5.5
18 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/215,649A
21 FILING DATE: 17-Dec-1998
22 CLASSIFICATION: <Unknown>
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/996,139
26 FILING DATE: <Unknown>
27 APPLICATION NUMBER: USSN 08/813,509
28 FILING DATE: 07 MARCH 1997
29 APPLICATION NUMBER: USSN 08/772,330
30 FILING DATE: 23 DECEMBER 1996
31
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Perkins, Patricia Anne
34 REGISTRATION NUMBER: 34,693
35 REFERENCE/DOCKET NUMBER: 2851-A
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (206)587-0430
38 TELEFAX: (206)233-0644
39
40 INFORMATION FOR SEQ ID NO: 12:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 954 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: cDNA
47 HYPOTHETICAL: NO
48 ANTI-SENSE: NO
49 ORIGINAL SOURCE:
50 ORGANISM: Homo sapiens
51 IMMEDIATE SOURCE:
52 LIBRARY: <Unknown>
53 CLONE: hURANKL (full length)
54
55 FEATURE:
56 NAME/KEY: CDS
57 LOCATION: 1..951
58
59 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
60 US-09-215-649A-12
61
62 Query Match 100.0% Score 954: DB 4: Length 954:
63 Best Local Similarity 100.0%: Prid. NO. 2.5e-251:
64 Matches 954: Conservative 0: Mismatches 0: Indels 0: Gaps 0
65
66 1 ATGCGCGCGCGCAGAGAGACTACCAAGTACCTGCGCTCGAGAGAGATGGCGGC 60
67 1 ATGCGCGCGCGCAGAGAGACTACCAAGTACCTGCGCTCGAGAGAGATGGCGGC 60
68
69 61 GGGCGCGGAGCGCGCGCAGAGAGAGGGCCCCCTGCGACGCGCCCGCGCGCTGCGGACAG 120
70 61 GGGCGCGGAGCGCGCGCAGAGAGAGGGCCCCCTGCGACGCGCCCGCGCGCTGCGGACAG 120
71
72 121 CCCCCCGCGCGCTCCGCTCATGTTTCGTGGCGCTCTGAGGCTGGGGCTGGGCGCAGGTT 180
73 121 CCCCCCGCGCGCTCCGCTCATGTTTCGTGGCGCTCTGAGGCTGGGGCTGGGCGCAGGTT 180
74
75 Db 121 CCCCCCGCGCGCTCCGCTCATGTTTCGTGGCGCTCTGAGGCTGGGGCTGGGCGCAGGTT 180

```


REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 158..1105
US-08-842-842-6

Query Match 69.8%; Score 666.2; DB 2; Length 2295;
Best Local Similarity 82.5%; Pred. No. 1.5e-172;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

QY 1 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGCTCGGAGAGATGGCGGC 60
DB 158 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGCTCGGAGAGATGGCGGC 217
QY 61 GGGCCCGGAGGCGCGAGAGGCGCCCTGACAGCGCCGCGC---CGCGCGCTCGCGCGC 117
DB 218 GGGCCCGGAGGCGCGAGAGGCGCCCTGACAGCGCCGCGCGCTCTTGACACGGCTCGGCG 277
QY 118 CAGCCCGCGCGCGCTCCGCTCCATGTTCTGCGCCCTCGGCGCTGCGCGCAG 177
DB 278 CCGCGACCGCGCGCTCCGCTCCATGTTCTGCGCCCTCGGCGCTGCGCGCAG 337
QY 178 GTTGTCTGAGAGGTGCGCTGTTCTCTATTTCAGAGCGCAGATGATCTATAGATA 237
DB 338 GTTGTCTGAGAGGTGCGCTGTTCTCTATTTCAGAGCGCAGATGATCTATAGATA 397
QY 238 TCAGAGATGAGACTGACTGACTATTTATAGATTTAGACTCAGTCAAGTATGATTT 297
DB 398 TCAGAGATGAGACTGACTGACTATTTATAGATTTAGACTCAGTCAAGTATGATTT 457
QY 298 CAGAGACACTCTGAGAGTCAAGATACAAATTAATCTGATTCATGTAAGAGATT 357
DB 458 CAGAGACTGACTCTGAGAGTCAAGATACAAATTAATCTGATTCATGTAAGAGATT 511
QY 358 AAGAGCGCTTTCAAGAGACTGTCAGAAAGGAATTACAAATATCGTTGGATCAGCAG 417
DB 512 AAGAGCGCTTTCAAGAGACTGTCAGAAAGGAATTACAAATATCGTTGGATCAGCAG 571
QY 418 ATCAGAGCAGAGAAAGCATGTGTGATGCTCATGTGATCTGAGATCTGCGCAAGAGAGC 477
DB 572 TTCTCAGAGAGCTCCAGCTATGATGGAAGGCTCATGTGATGATGTCGCCAGAGGCAAG 631
QY 478 CTGGAAGCTCAGCGCTTTGCTGCTCATCTCATATTAATGCCACCAATCCCATGCTGTC 537
DB 632 CCGTGAAGCGCTCAGCTATGATGGAAGGCTCATGTGATGATGTCGCCAGAGGCTGTC 691
QY 538 CATAAAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
DB 692 CATAAAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
QY 598 ACTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 657
DB 752 ACTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 811
QY 658 ATTGCTTTGAGATCATGTAAGTCTGAGAGACTGACTGACTGACTGACTGACTGACTG 717
DB 812 ATTGCTTTGAGATCATGTAAGTCTGAGAGACTGACTGACTGACTGACTGACTGACTG 871
QY 718 GTGAGTCACTAAACACCATATCAAAATCCAAAGTCTATACCCGATGAAGAGAGA 777
DB 872 GTGAGTCACTAAACACCATATCAAAATCCAAAGTCTATACCCGATGAAGAGAGA 931
QY 778 AGCAGCAAGTATGTTGAGAGGATTTGGAATTCATTTTATTCATTAAGCGTTGGTGA 837
DB 932 AGCAGCAAGTATGTTGAGAGGATTTGGAATTCATTTTATTCATTAAGCGTTGGTGA 991

QY 838 TTTTAACTAGAGGTCTGAGAGAGAAATCAGCATCCAGGCTCTCCACCCCTCTACTG 897
DB 992 TTTTAACTAGAGGTCTGAGAGAGAAATCAGCATCCAGGCTCTCCACCCCTCTACTG 1051
QY 898 GATCCGAGTACAGATGCAACATACCTTTGGGCTTTTAAAGTTCAGATATATGATGA 954
DB 1052 GATCCGAGTACAGATGCAACATACCTTTGGGCTTTTAAAGTTCAGATATATGATGA 1108

RESULT 7
US-09-052-521C-1
Sequence 1, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Bv
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: US/09/052,521C
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2295
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (158)..(1105)
US-09-052-521C-1

Query Match 69.8%; Score 666.2; DB 4; Length 2295;
Best Local Similarity 82.5%; Pred. No. 1.5e-172;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

QY 1 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGCTCGGAGAGATGGCGGC 60
DB 158 atgcgccgcgccagagagactacaccaagtacctgctcgagagatggcggc 217
QY 61 GGGCCCGGAGGCGCGAGAGGCGCCCTGACAGCGCCGCGC---CGCGCGCTCGCGCGC 117
DB 218 gggcccgagcgccag 277
QY 118 CAGCCCGCGCGCGCTCCGCTCCATGTTCTGCGCCCTCGGCGCTGCGCGCAG 177
DB 278 cggcgccgcgcgcgctcccgctccatggttctgctcgagagagagagagagagagag 337
QY 178 GTTGTCTGAGAGGTGCGCTGTTCTCTATTTCAGAGCGCAGATGATCTATAGATA 237
DB 338 gttgtctgagaggtgcgctgttctctattttcagagcgccagatgattatagata 397
QY 238 TCAGAGATGAGACTGACTGACTATTTATAGATTTAGAGTTCAGTCAAGTATGATTT 297
DB 398 tcagagatgagactgactgactatttatagattttagagttcagatgattatgata 457
QY 298 CAGAGACAACTCTGAGAGTCAAGATACAAATTAATACCTGATTCATGTAAGAGATT 357
DB 458 cagagacaaactctgagagtgagagagagagagagagagagagagagagagagagag 511
QY 358 AAGAGCGCTTTCAAGAGAGTGTGCAAAAGGAATTACAAATATCGTTGGATCAGCAG 417
DB 512 aagagcgctttcaagagagtggtgcaaaaggattacaaatattcgttggatcagcag 571
QY 418 ATCAGAGCAGAGAAAGCATGTGTGATGCTCATGTGATCTGAGATCTGCGCAAGAGCAG 477
DB 572 ttctcagagagctcagctatgagagagagagagagagagagagagagagagagagag 631
QY 478 CTGGAAGCTCAGCGCTTTGCTCATCTCATATTAATGCCACCAATCCCATCTGCTGTC 537

| | | | |
|----|------|--|------|
| Db | 632 | ccctgaagcccgccacattctgcacacactccatcaatctctgcacgaatcccatcggtctcc | 631 |
| OY | 538 | CATTAAGTGAAGTCTGTCTCTCTGTGGTACCATGATCGGGTTTGGGCGAAGATCTCCAAATG | 537 |
| Db | 692 | cataaagtaactctctctctctctgttaccacgaatcgcgagctcgggccaaatctctaaatg | 751 |
| OY | 598 | ACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTAATTAACCTGTAATGCCAAC | 657 |
| Db | 752 | acgttaagcaaacggaataaataaggtttaacaagaatgtctctcatctaccctgaagcaac | 811 |
| OY | 658 | ATTTCGTTTGACATTCATGTAACCTTCAGGAGACCTACTACTACAGATATCTTCAACTAATG | 717 |
| Db | 812 | attctgccttcgcacatcagaaacatcgggaagcgttacctacagaactctcttcagctatg | 871 |
| OY | 718 | GTTACGCTCACTAAACACACATCAAAATCCGAAGTTCTATACCCGTGAAGAAGAGA | 777 |
| Db | 872 | gtctatgtctgttaaaaccacgacataaaatcccaagttctcataaactgtatgaaagaagaag | 931 |
| OY | 778 | AGCACCAAGATTGTGTCAGGGAATTTCTGAATTCATTTTAAATTCATAAACGTTGTGTGA | 837 |
| Db | 932 | agcagaaaaaacctgtctgggcaattctgaaattccaaacttattccataaattglttgggga | 991 |
| OY | 838 | TTTTTTTAAGTTACGGCTTGGAGAGAAATCAGATCGAGGCTTCACACCCCTCTTAATCG | 897 |
| Db | 992 | tcttctcaagctcccgagctctgtgaaagaattatgacatcaagttgtccaacccctccctctg | 1051 |
| OY | 898 | GATCCGGATCGAGTGCACAACTACTTTGGGGCTTTTAAAGTTGCAGATATAGATTGA | 954 |
| Db | 1052 | gattccggatccaaagttcgcgaagtaactcttggggcttctcaaaatctaaagttcaagataagactba | 1108 |

RESULT 8
 US-08-996-139-10
 : Sequence 10, Application US/08996139
 : Patent No. 6017729
 : GENERAL INFORMATION:
 : APPLICANT: Anderson, Dirk M.
 : APPLICANT: Gallbert, Laurent
 : APPLICANT: Maraskovsky, Eugene
 : TITLE OF INVENTION: Receptor Activator of NF-kappaB
 : NUMBER OF SEQUENCES: 19
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Immune Corporation, Law Department
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: WA
 : COUNTRY: USA
 : ZIP: 98101
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: Apple Power Macintosh
 : OPERATING SYSTEM: Apple Operating System 7.5.5
 : SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/996,139
 : FILING DATE: 22 DECEMBER 1997
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: USSN 60/064,671
 : FILING DATE: 14 OCTOBER 1997
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: USSN 08/813,509
 : FILING DATE: 07 MARCH 1997
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: USSN 08/772,330
 : FILING DATE: 23 DECEMBER 1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Perkins, Patricia Anne
 : REGISTRATION NUMBER: 34,693
 : REFERENCE/DOCKET NUMBER: 2851-A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (206)587-0430

```

TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO.: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY:
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
US-08-996-139-10

```

| Query Match | 64.5% | Score 615 | DB 3 | Length 1630 |
|-----------------------|--|--------------------|----------|-------------|
| Best Local Similarity | 82.2% | Pred. No. 1.3e-158 | | |
| Matches 734 | Conservative 0 | Mismatches 150 | Indels 9 | Gaps 2 |
| QY | CCGAGACCCCGCAGAGAGGCCCCCTGACAGGCCCGC---CGCGCGCTGGCGCCGACACAGC | 121 | | |
| Db | 1 CCGGGCTCCCAACAGAGAGGTCCGGTCGACACCCGGCCCTTCTGACACCGCTCCGGGGCGCC | 60 | | |
| QY | 122 CCCCCCGCCCTCCCGCTCCATGTTTCGTGGCCCTCTCGGGGCTGGGGCTGGGCCAGTTTG | 181 | | |
| Db | 61 CACCCGCGCCCTCCCGCTCCATGTTTCGTGGCCCTCTCGGGGCTGGGGAGCTGGGCCAGTTGG | 120 | | |
| QY | 182 TCTGAGGCTGGCCCTGTCTTCTTATTTTCAGAGCCAGATGGAATCTTAATAGAAATATCG | 241 | | |
| Db | 121 TCTGAGAGATGCTCTGTCTTCTTCTTCTTTCAGGCCAGATGGAATCTTAATAGAAATATCG | 180 | | |
| QY | 242 AAGATGGCACTCACTGCATTTTATAGAAATTTTGGAGCTCCATGAAATGAGATTTTTCAG | 301 | | |
| Db | 181 AAGACAGCACTCACTGCCTTTTATAGAAATCTTGGAGCTCCATGAAATGAGATTTTTCAG | 240 | | |
| QY | 302 ACACACTCTGGAGAGTCAAGATACAAATTAATCTGATTCATGTAGAAATTAAC | 361 | | |
| Db | 241 ACTGCACCTCTGGAGAGTCAAGACAC-----ACTACCTGCATCTTCGAGAGAGATGAAC | 294 | | |
| QY | 362 AGGCTTTTCAAGGAGCTCTGCCAAAGAAATTCACAACTATCGTTGGATCAGACACATCA | 421 | | |
| Db | 295 AAGCTTTTTCAGGGGGCCCTGAGAAAGAACTGCAACACTTTTGGGGCCAGCGCTTCT | 354 | | |
| QY | 422 GAGCAGAAAGACGATGGTGATGGCTCATATGGTATGCTGGCCAAAGACGACCAAGCTTG | 481 | | |
| Db | 355 CAGGAGCTTCACACTATGATGGAAGGCTCATGTGTTGGATGTGGCCCAAGGACCAAGCTTG | 414 | | |
| QY | 482 AAGCTCAGCCTTTTGTCTCATCTCACTATTATGCCACCGACATCCCATCTGGTCCCATTA | 541 | | |
| Db | 415 AGGCCACACCAATTTGCACACCTCACCATCAATATGCTGCAGCATCCCATCGGGTCCCATTA | 474 | | |
| QY | 542 AAGTAGCTGTGCTCTTGTGTACCATGATCGGGGTTGGGCCCAAGATCTTCAACATGACTT | 601 | | |
| Db | 475 AAGTAGCTGTGCTCTTGTGTACCAAGATCGAGGCTGGGCCCAAGATCTTCAACATGACTT | 534 | | |
| QY | 602 TTAGCAATGGAATAATAGTTAATTCAGAGATGGGCTTTTATACCTGTATGCAACATTT | 661 | | |
| Db | 535 TTAGCAAGGGAATAATAGGTTTAAACCAAGATGGCTTCTATTACCTGTATGCAACATTT | 594 | | |
| QY | 662 GCTTTGCATTCATGAAACTTCAGGAGACCTAGCTACAGAGATATCTTCAACTAATGTGT | 721 | | |
| Db | 595 GCTTTGCATTCATGAAACTTCGAGAGACCTAGCTACAGATATCTTCAAGCTGATGTGT | 654 | | |
| QY | 722 ACGTCACATAAAACCGACATCAAAATCCCAAGTTCTCATACCTGATGAAAGGAGAGACA | 781 | | |
| Db | 655 ATGTCGTTAAACCGACATCAAAATCCCAAGTTCTCATACCTGATGAAAGGAGAGAGACA | 714 | | |


```

; SEQ ID NO 10
; LENGTH: 759
; TYPE: DNA
; ORGANISM: synthetic fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(759)
;
US-09-320-424-10

```

| | | | | |
|---------------------------|--------|------------------|-----------|-------------|
| Query Match | 7.3%; | Score 69.4; | DB 4; | Length 759; |
| Best Local Similarity | 51.9%; | Pred. No. 1e-09; | | |
| Matches 182; Conservative | 0; | Mismatches 166; | Indels 3; | Gaps 1. |

| | | | |
|----|-----|--|-----|
| QY | 591 | CACATGACTTTTGGCATGGAAGAAACATATGTATATCAGATGGCTTTATTAACCGTA | 650 |
| Db | 411 | caacttgaacttgggaatgggttgaacttgcgttccatcgaaagggcttttactacatcta | 470 |
| QY | 651 | TGCCAACATTTTGCTTCACATCATGTGAACATCTCAGGAGACCTACCTCAGAGATCTTCA | 710 |
| Db | 471 | ttcccaacaactacttgcgtatcttgcgggaataataaga---aaacacaagaacgcgaa | 527 |
| QY | 711 | ACTATGSGTGTACGTCACATAAACCAGCATCAAAATCCCAAGTTTCATACCTGATGAA | 770 |
| Db | 528 | acaatgtgtccaatatatttacaataatacacaagtatcccgacctatattgttgaagaa | 587 |
| QY | 771 | AGGAGGAAGCCACCAAGTATTGGTCAGGGAATTCGTGAATTCATTTTATTCACATAACGT | 830 |
| Db | 588 | aagtcgtagaataagtgtgtgtctaaagaatgcagaaatatagnaactatccatcatca | 647 |
| QY | 831 | TGCTGGATTTTAACTTAAGTACGSTCTGAGAGAGAAATCGATCGACGGCTCCACCCCTC | 890 |
| Db | 648 | aggggggaatattttagctctaaagaaatgacagaatcttgcgttctcgttaacaatagaca | 707 |
| QY | 891 | CTTACGCGATCCGATCGATCGAGATGCACACATATCTTGGGCTTTTAAAGTTCG | 941 |
| Db | 708 | cttgaagaacatgagcaatgaaagccagtttcttggggcccttttaagtgtg | 758 |

RESULT 12
US-09-320-424-12
; Sequence 12, Application US/09320424

?
 ? APPLICANT: Wiley, Steven R.
 ? APPLICANT: Goodman, Raymond G.
 ? TITLE OF INVENTION: Cytokine that Induces Apoptosis
 ?
 ? FILE REFERENCE: 2835-E
 ? CURRENT APPLICATION NUMBER: US/09/320,424
 ?

```

1 EARLIER APPLICATION NUMBER: 09/190,046
2 EARLIER FILING DATE: 1998-11-10
3 EARLIER APPLICATION NUMBER: 09/048,644
4 EARLIER FILING DATE: 1998-03-26
5 EARLIER APPLICATION NUMBER: 08/670,354
6 EARLIER FILING DATE: 1996-06-25
7 EARLIER APPLICATION NUMBER: 08/548,366
8 EARLIER FILING DATE: 1995-11-01
9 EARLIER APPLICATION NUMBER: 08/496,633
10 EARLIER FILING DATE: 1995-06-29
11 NUMBER OF SEQ ID NOS: 25
12 SOFTWARE: Patent Ver. 2.0

```

```

; SEQ ID NO 12
; LENGTH: 768
; TYPE: DNA
; ORGANISM: synthetic fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
DS-09-320-424-12

```

| | |
|-------------|-------------------------------------|
| query match | 7.3%; Score 69.4; DB 4; Length 768; |
|-------------|-------------------------------------|

Best Local Similarity 51.9%; Pred. No. 11e-09;
Matches 182; Conservative 0; Mismatches 166; Indels 3; Gaps 1

| | | | |
|-----|-----|--|-----|
| bby | 591 | CACATGACTCTTTAGCATAAAGAAAACTATATAGTAAATCAGATGGCTTTATTACCTGTGA | 650 |
| bby | 420 | caacttccactctgaagaaayggytgacatcggcatcca tyaanaagyggttttaactaatctca | 479 |
| bby | 651 | TGCCAACAATTTGGTTTTGCAGATCATGAATGAACCTTCAGAGACCCTAGCTACAGATATCTTCA | 710 |
| bdb | 480 | tccccaacatactatttcgcatttcgaattccaggaggaataaaga---aaacaagaagacgaaa | 536 |
| bby | 711 | ACTAATGTTGTACGTCATPAAACCCAGCATCAAATCCCAAGTCTCTATACCGTGATGA | 770 |
| bby | 537 | acaatatgtccaatatataattacaataacaaagtatcttcgacctaatatytitgagaa | 596 |
| bdb | 771 | AGGAGGAAGACCAACAAGTATTTGGTCAGGGAGATTCGAAATTCATTTTATTCGCATAAAGC | 830 |
| bby | 597 | aagtcgtacgaataatagtttgttgcgtctaagaatgcagaaataatgacatacttcatactca | 656 |
| bdb | 831 | TGGTGGATTTTTTAAGTTACGGCTCTGAGAGAAGAAATCAAGATCGAGTCTCCACCCCCTC | 890 |
| bby | 657 | agggggagaatcttgaagcttaagaaaaatgacagaatllttgttctcgtlaaacaatagsgca | 716 |
| bdb | 891 | CTTACTGGATCCGATCCAGGATCCAACATACTTTGGGCTTTTAAAGTTGC | 941 |
| bby | 717 | ctgatagacaatgacacatgaagcacggttttttcggcgcccttttagttg | 767 |

RESULT 13
US-08-584-031-2
Sequence 7 Application HS/08584031A

Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.220S03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-584-031-2

```

| | | | | |
|-----------------------|--------------|--------------------|-----------------|--------------|
| Query Match | 7.38; | Score 69.4; | DB 3; | Length 1042; |
| Best Local Similarity | 51.9%; | Pred. No. 1.2e-09; | | |
| Matches 182; | Conservative | 0; | Mismatches 166; | Indels 3; |
| | | | Gaps | 17; |

| | | | |
|----|-----|---|-----|
| QY | 591 | CAACATGACTTTTGGCANTGGAAACCAATAGTTATCGAGATGGCTTTTATCCGTGA | 650 |
| | | | |
| Db | 585 | caacttgcactcttgagaatgylgacacggycacacccatgaaaagyltttctctaccta | 644 |
| | | | |
| QY | 651 | TGCCAACATTGGCTTGTGAGATCATGAACTTCAGAGACCTAGCTACAGATATTCTCA | 710 |
| | | | |
| Db | 645 | tcccaacaacactcttcttgattccagggggaataaaga---aaacaagaacgacaa | 701 |
| | | | |
| QY | 711 | ACTAATGGTGAACGTACATTAACCCAGATTCATACCGATTCATACCGATTCAT | 770 |
| | | | |
| Db | 702 | acaaatgycacaaatatatttccaatacacaagttaacctacatatattgtcagaa | 761 |
| | | | |
| QY | 771 | AGAGAGAGACCAACGAATGTTGTGAGGATTTGTGAATTCATTTTATTCATTAACGT | 830 |
| | | | |
| Db | 762 | aagtcgtagaataattgtctgtcctaagatctgagaatatgtgacctcttccatcatca | 821 |
| | | | |
| QY | 831 | TGTTGATATTTTAAATTAACGGTCTGGAGAGAAATCACATCGAGGTCTCCAAACCTC | 890 |
| | | | |
| Db | 822 | aagggggaatatttgcgtctaaggaanaatgacagaatttctgtctctgtacaacaaatgaca | 881 |
| | | | |
| QY | 891 | CTTACTGATCCGATCGAGATCAACATATCTTTGGGGCTTTTAAAGTCGC | 941 |
| | | | |

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 8, 2002, 20:05:54 ; Search time 89.9 seconds

(without alignments)
391.662 Million cell updates/sec

Title: US-09-865-363-13

Perfect score: 1685
Sequence: 1 MRRASRDYRKYLRGSEEMG.....LDDPDQATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:.*
1: /SID55/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID55/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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11: /SID55/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID55/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID55/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID55/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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19: /SID55/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID55/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID55/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID55/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1685 | 100.0 | 317 | AAW83195 | Human osteoprotege |
| 2 | 1685 | 100.0 | 317 | AAW69957 | NE-KB receptor act |
| 3 | 1685 | 100.0 | 317 | AAW68293 | NE-KB receptor act |
| 4 | 1685 | 100.0 | 317 | AAW84417 | Amino acid sequenc |
| 5 | 1685 | 100.0 | 317 | AAE08738 | Human receptor act |
| 6 | 1685 | 100.0 | 317 | AAE04426 | Human receptor act |
| 7 | 1685 | 100.0 | 317 | AAE01993 | Human full-length |
| 8 | 1677 | 99.5 | 317 | AAW83018 | Osteoclastogenesis |
| 9 | 1417.5 | 84.1 | 316 | AAW83194 | Human osteoprotege |
| 10 | 1417.5 | 84.1 | 316 | AAW83017 | Osteoclastogenesis |
| 11 | 1417.5 | 84.1 | 316 | AAW59654 | Amino acid sequenc |

| | | | | | |
|----|--------|------|-----|----------|--------------------|
| 12 | 1417.5 | 84.1 | 316 | AAV17874 | Murine TRANCE. Mu |
| 13 | 1417.5 | 84.1 | 316 | AAV91024 | Mouse OBM protein |
| 14 | 1417.5 | 84.1 | 316 | AAW84418 | Amino acid sequenc |
| 15 | 1417.5 | 84.1 | 316 | AAW84419 | Amino acid sequenc |
| 16 | 1396.5 | 82.9 | 318 | AAW82092 | Rat osteoclast dif |
| 17 | 1326.5 | 78.7 | 294 | AAW69956 | NE-KB receptor act |
| 18 | 1326.5 | 78.7 | 294 | AAW68292 | NE-KB receptor act |
| 19 | 1326.5 | 78.7 | 294 | AAE08737 | Murine receptor ac |
| 20 | 1326.5 | 78.7 | 294 | AAE04425 | Murine receptor ac |
| 21 | 1326.5 | 78.7 | 294 | AAE01992 | Murine RANKL (rege |
| 22 | 1294 | 76.8 | 246 | AAW83020 | Osteoclastogenesis |
| 23 | 1293 | 76.7 | 245 | AAV17873 | Human TRANCE. Hom |
| 24 | 1136 | 67.4 | 501 | AAW84420 | Amino acid sequenc |
| 25 | 1109 | 65.8 | 244 | AAW83019 | A murine OCIF-bind |
| 26 | 852 | 50.6 | 160 | AAW80273 | Amino acid sequenc |
| 27 | 814 | 48.3 | 152 | AAW67248 | Human RANKL. Homo |
| 28 | 790 | 46.9 | 170 | AAW08386 | Mouse FLAG-murine |
| 29 | 771 | 45.8 | 187 | AAW84420 | Amino acid sequenc |
| 30 | 769 | 45.6 | 173 | AAW84421 | Amino acid sequenc |
| 31 | 768 | 45.6 | 160 | AAW80272 | Amino acid sequenc |
| 32 | 759 | 45.0 | 173 | AAW84422 | A murine osteoprot |
| 33 | 721.5 | 42.8 | 188 | AAW84423 | An osteoprotegerin |
| 34 | 711.5 | 42.2 | 182 | AAW84424 | An osteoprotegerin |
| 35 | 691 | 41.0 | 173 | AAW84425 | DNA encoding osteo |
| 36 | 683 | 40.5 | 139 | AAW91023 | Mouse OBM protein |
| 37 | 670 | 39.8 | 173 | AAW84426 | An osteoprotegerin |
| 38 | 317.5 | 18.8 | 74 | AAV91020 | Mouse OBM protein |
| 39 | 252.5 | 15.0 | 281 | AAV27016 | Human Apo-2 ligand |
| 40 | 252.5 | 15.0 | 281 | AAV27017 | Human Apo-2 ligand |
| 41 | 251.5 | 14.9 | 279 | AAW76332 | Human TLR2 (TRAIL) |
| 42 | 251.5 | 14.9 | 279 | AAW5032 | Tumour necrosis fa |
| 43 | 251.5 | 14.9 | 281 | AAW27134 | Human Apoptosis in |
| 44 | 251.5 | 14.9 | 281 | AAW19787 | Human Apoptosis in |
| 45 | 251.5 | 14.9 | 281 | AAW19777 | Novel cytokine Apo |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| AAW83195 | AAW83195 standard; Protein: 317 AA. |
| XX | |
| AC | AAW83195; |
| XX | |
| DT | 11-FEB-1999 (first entry) |
| XX | |
| DE | Human osteoprotegerin binding protein from the pcDNA/huOPCbp1.linsert. |
| XX | |
| KW | Human; osteoprotegerin binding protein; OPG binding protein; arthritis; |
| KW | osteoporosis; osteoclast maturation; bone disease; metastasis; OMR; |
| KW | hypercalcaemia; osteoclast differentiation and activation receptor; |
| KW | Paget's disease. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | W09846751-A1. |
| XX | |
| PD | 22-OCT-1998. |
| XX | |
| PE | 15-APR-1998; 98WO-US07584. |
| XX | |
| PR | 30-MAR-1998; 98US-0052521. |
| PR | 16-APR-1997; 97US-0842842. |
| PR | 23-JUN-1997; 97US-0880855. |
| XX | |
| PA | (AMGE-) AMGEN INC. |
| XX | |
| PI | Boyle WJ; |
| XX | |
| DR | WPI: 1998-594578/50. |
| DR | N-PSDB; AAV70285. |
| XX | |

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis

PS Claim 19; Fig 4; 47bp; English.

XX The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OPG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.

XX Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 19; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRRASRDYTKYLRGSEENGSGPAGHNEPPLNAPPPAHOPPAARSFVALGIGLGOV 60
 DB 1 mrrasrdytkylrgseengsgpaghneppahpppaaarsmtfvallgiglv 60
 OY 61 VCSVALFFYFRAQMPNRISEDTGTCIYRIILAHENADFOTTLRSOPTKLIPDSCRIRK 120
 DB 61 vcsvalffyfraqmnpriisedgtctcyrlirlnhenadfttlesqdtklipdscriik 120
 OY 121 QAFQAVOKELQIHIVGSHIRAEKAMVDGSWDLAKRSKLEQAPPAHLTINATDIPSGSH 180
 DB 121 qafqavokelqihivsgshiraeakamvdsdlakrskleaqppahltinatdipsgh 180
 OY 181 KVSLSWYHIDRGWAKISNMTFNSGKLIYNQGFYLYANICRHNHETSGDLATEYLQIMV 240
 DB 181 kvslswyhidrgwakismtfsngklyvngdfylyanlcrhnetsgdlateylqimv 240
 OY 241 VYTKSIRKIPSSHTLMKSGSTKYWGNSGFHFYSINVGCFELRSGEETISIEVSNPSPILD 300
 DB 241 vytksirkipsshtlmksgstkywgsnsefhfysinvgfflirsgeelstevsnpslld 300
 OY 301 PDQATYFGAEKVRDID 317
 DB 301 pdqatyfgaekvridd 317

RESULT 2

AAW69957
 ID AAW69957 standard; Protein; 317 AA.

XX AAW69957;

XX 08-OCT-1998 (first entry)

XX NF-kB receptor activator RANK ligand (RANKL).

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

XX immune response; inflammatory response; toxic shock; sepsis;

XX RANKL; RANK ligand; tumour necrosis factor; TNF.

XX Homo sapiens.

XX W09828426-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23775.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

XX (IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI: 1998-377657/32.

XX DR N-PSDB; AAW41378.

XX New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells

PS Claim 27; Pages 59-60; 80pp; English.

XX This represents a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

XX Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 19; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRRASRDYTKYLRGSEENGSGPAGHNEPPLNAPPPAHOPPAARSFVALGIGLGOV 60
 DB 1 mrrasrdytkylrgseengsgpaghneppahpppaaarsmtfvallgiglv 60
 OY 61 VCSVALFFYFRAQMPNRISEDTGTCIYRIILAHENADFOTTLRSOPTKLIPDSCRIRK 120
 DB 61 vcsvalffyfraqmnpriisedgtctcyrlirlnhenadfttlesqdtklipdscriik 120
 OY 121 QAFQAVOKELQIHIVGSHIRAEKAMVDGSWDLAKRSKLEQAPPAHLTINATDIPSGSH 180
 DB 121 qafqavokelqihivsgshiraeakamvdsdlakrskleaqppahltinatdipsgh 180
 OY 181 KVSLSWYHIDRGWAKISNMTFNSGKLIYNQGFYLYANICRHNHETSGDLATEYLQIMV 240
 DB 181 kvslswyhidrgwakismtfsngklyvngdfylyanlcrhnetsgdlateylqimv 240
 OY 241 VYTKSIRKIPSSHTLMKSGSTKYWGNSGFHFYSINVGCFELRSGEETISIEVSNPSPILD 300
 DB 241 vytksirkipsshtlmksgstkywgsnsefhfysinvgfflirsgeelstevsnpslld 300
 OY 301 PDQATYFGAEKVRDID 317

```

Db      301  pdqdaelyfgafkvrld 317
      |||
RESULT  3
ID      AAM68293 standard; Protein: 317 AA.
AC      AAM68293;
XX      08-OCT-1998 (first entry)
XX      NF-kB receptor activator RANK ligand (RANKL).
XX      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX      immune response; inflammatory response; toxic shock; sepsis;
XX      RANKL; RANK ligand; tumour necrosis factor; TNF.
XX      Homo sapiens.
XX      MO9828424-A2.
XX      02-JUL-1998.
XX      22-DEC-1997; 97MO-US23866.
XX      14-OCT-1997; 97US-0064671.
XX      23-DEC-1996; 96US-0059978.
XX      07-MAR-1997; 97US-0813509.
XX      (IMMV ) IMMUNEX CORP.
XX      Anderson DM, Galibert LJ, Maraskovsky E;
XX      MPI: 1998-377655/32.
XX      N-PSDB: AAV41372.
XX      New isolated receptor activator of necrosis factor-kappa B - useful
XX      for, e.g. developing products for regulating an immune or
XX      inflammatory response, treating toxic shock or sepsis
XX      Example 7: Pages 59-60; 80pp; English.
XX      This represents a human RANKL, a ligand for the RANK (receptor
XX      activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
XX      member of the tumour necrosis factor (TNF) family. Host cells transformed
XX      or transfected with an expression vector comprising the RANK encoding
XX      nucleic acid can be used to produce recombinant RANK protein. The soluble
XX      RANK may be used for inhibiting activation of NF-kB by contacting a cell
XX      expressing membrane-associated RANK with a soluble RANK which binds to
XX      RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
XX      used for regulating an immune or inflammatory response. Inhibition of
XX      NF-kB by RANK antagonists may be useful in ameliorating negative effects
XX      of an inflammatory response that result from triggering of RANK, e.g. in
XX      treating toxic shock or sepsis, graft-versus-host reactions, or acute
XX      inflammatory reactions. They can also be used in adjunct therapy for
XX      disease characterised by neoplastic cells that express RANK. The products
XX      can also be used for detection and drug screening.
XX      Sequence 317 AA:
XX
Query Match      100.0%; Score 1685; DB 19; Length 317;
Best Local Similarity 100.0%; Pred. No. 2,6e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      121  OAFQAVOKELQHTVIGSOHTRAEKAWYDGSWLDIAKRSKLEAOPFAHLLTNATDIPSGSH 180
      |||
Db      121  qafgavqkeiqhivsqhtraekamwgswlidlakrskleaqpfahlltnatdipsgsh 180
OY      181  KVSLSWYHDRGMAKISNMTFSGNKLIVNODGFYYLANICFRHHETSGDLATFYLQLMV 240
      |||
Db      181  kvslsswyhdtgrwakiannmtfsgnkllvngdgfylyanlcfrhethetsgdlatfeylqlmv 240
OY      241  YVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHYSINVGGEFKLRSGEISIEVSNPSILD 300
      |||
Db      241  yvktstiklpsshltlmkgselkwsygnsefhfysinvgffklrsgelsievsnpalld 300
OY      301  PDODATYEGAFKVRDID 317
      |||
Db      301  pdqdaelyfgafkvrld 317
RESULT  4
ID      AAY84417 standard; Protein: 317 AA.
AC      AAY84417;
XX      25-JUL-2000 (first entry)
XX      Amino acid sequence of a human osteoprotegerin ligand (OPGL).
XX      Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
XX      tumour necrosis factor receptor; type II transmembrane protein;
XX      osteoclast differentiation; CSF-1; osteoclast activator;
XX      immune response; osteoporosis; bone resorption.
XX      Homo sapiens.
XX      OS
XX      Key      Location/Qualifiers
XX      FH      Region      49..69
XX      FT      /note="Transmembrane region"
XX      FT      Domain      70..157
XX      FT      /note="extracellular stalk domain"
XX      FT      Region      158..317
XX      FT      /note="active ligand moiety"
XX      PN      WO200015807-A1.
XX      PD      23-MAR-2000.
XX      PF      13-SEP-1999; 99MO-DK00481.
XX      PR      15-SEP-1998; 98DK-0001164.
XX      PR      02-OCT-1998; 98US-0102896.
XX      PA      (MEBI-) M & E BIOTECH AS.
XX      PI      Halkier T, Haanling J;
XX      DR      MPI: 2000-271444/23.
XX      DR      N-PSDB: AAZ99964.
XX      PT      In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX      to treat, prevent and ameliorate osteoporosis.
XX      Claim 19: Page 78-79; 110pp; English.
XX      The present sequence represents a human osteoprotegerin ligand (OPGL).
XX      Osteoprotegerin is a secreted member of the tumour necrosis factor
XX      receptor family, which blocks osteoclastogenesis in a dose dependent
XX      manner. The OPGL protein is synthesised as a type II transmembrane
XX      protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
XX      is a potent osteoclast differentiation factor when combined with CSF-1.
XX      It is not capable of inducing osteoclast differentiation in the absence
XX      of CSF-1. OPGL is also an activator of mature osteoclasts. The
XX      specification describes a method for the in vivo down-regulation of

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RESULT 6
AAE04426
ID AAE04426 standard; Protein: 317 AA.
AC AAE04426;
XX
XX
DT 04-SEP-2001 (first entry)
XX
XX Human receptor activator of NF-chl B ligand (huRANKL) protein.
XX
XX Human: receptor activator of NF-chl B; RANK; tumour necrosis factor; TNF;
XX CD40; TNF receptor-associated factor; TRAF; ligand; Immune response;
XX Chromosome 10q22.1; huRANKL; chromosome 13q14; transmembrane protein.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 162..317
XX /note="Receptor binding region"
XX
XX US6242213-B1.
XX
XX 05-JUN-2001.
XX
XX 22-DEC-1997; 97US-0995659.
XX
XX 23-DEC-1996; 96US-0059978.
XX 07-MAR-1997; 97US-0077181.
XX 14-OCT-1997; 97US-0064671.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM;
XX
XX WPI: 2001-407216/43.
XX N-PSDB; AAD08715.
XX
XX New DNA molecules, useful for producing ligands (which are useful for
XX regulating immune response and in screening for inhibitors of NF-chl B
XX receptor activator) of the receptor activator of NF-chl B (RANK)
XX
XX Claim 1; Column 65-66; 43pp; English.
XX
XX The present invention relates to receptor activator of NF-chl B (RANK)
XX DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
XX chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
XX proteins respectively. RANK is a member of the tumour necrosis factor
XX (TNF) superfamily and it closely resembles CD40 in the extracellular
XX region. RANK associates with TNF receptor-associated factor (TRAF) 2
XX and TRAF3. The DNA molecules are useful for producing ligands of RANK.
XX The ligands are useful for regulating immune response and in screening
XX for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
XX protein.
XX
XX Sequence 317 AA:
XX
XX Query Match 100.0%; Score 1685; DB 22; Length 317;
XX Best Local Similarity 100.0%; Pred. No. 2, 6e-156;
XX Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 181 KVSLSWYHDSGNKISNMFPSNGKLIYNODGFYLYANICFRHHETSGDLATEYLQMV 240
DB 181 KVSLSWYHDSGNKISNMFPSNGKLIYNODGFYLYANICFRHHETSGDLATEYLQMV 240
QY 241 VYKTSIKIPSSHTLMKGSTKRYSGNSEHFYSINVGCFKLRSGEISIEVSNPGLD 300
DB 241 YVTKTSIKIPSSHTLMKGSTKRYSGNSEHFYSINVGCFKLRSGEISIEVSNPGLD 300
QY 301 PDDATYFGAKRYVDID 317
DB 301 PDGATYFGATKRYVDID 317
RESULT 7
AAE01993
ID AAE01993 standard; Protein: 317 AA.
AC AAE01993;
XX
XX 31-JUL-2001 (first entry)
XX
XX Human full-length RANKL (receptor activator of NF-kappab ligand).
XX
XX Human: receptor activator of NF-kappab; RANK; nuclear factor-kappab;
XX NF-kappab; tumour necrosis factor; TNF; type I transmembrane protein;
XX TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopetrotic;
XX inflammatory reaction; bone resorption; gene therapy; immunomodulator;
XX immune system dysfunction; familial expansile osteolysis; FEO;
XX early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.
XX
XX Homo sapiens.
XX
XX WO200136637-A1.
XX
XX 25-MAY-2001:
XX
XX 14-NOV-2000; 2000WO-US31459.
XX
XX 17-NOV-1999; 99US-0442029.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Hughes AE;
XX
XX WPI: 2001-329222/34.
XX N-PSDB; AAD05904.
XX
XX New DNA encoding a receptor activator of NF-kappab polypeptide for the
XX treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
XX
XX Disclosure: Page 76-77; 96pp; English.
XX
XX The present invention relates to a novel receptor, referred to as RANK
XX (receptor activator of NF (nuclear factor)-kappab), a member of TNF
XX (tumour necrosis factor) receptor superfamily. RANK is a type I
XX transmembrane protein that interacts with TNF receptor-associated
XX factors (TRAFs). Triggering of RANK by overexpression or co-expression
XX of the transmembrane bound RANK ligand (RANKL) results in upregulation
XX that is most extensively utilised in cells of the immune system.
XX Inhibition of NF-kappab by RANK antagonists is useful in ameliorating
XX negative effects of inflammatory reactions, and the effects of excess
XX bone resorption. The RANK DNA's, proteins and their analogues are useful
XX for the preparation of pharmaceutical compositions, for infecting target
XX cells for use in gene therapy applications in diagnosing diseases
XX associated with RANK, and as targets for use in screening assays. They
XX may be used in the treatment or diagnosis of immune system dysfunction.
XX The present invention also encompasses gene therapy methods to correct
XX gene-activating mutations, associated with e.g. familial expansile
XX osteolysis (FEO) and early onset Paget's disease of bone (EP). The
XX present amino acid sequence is full-length human RANKL (huRANKL)
XX protein. The RANKL gene is located in chromosome 13q14.

```

XX S0 Sequence 317 AA;
Query Match 100.0%; Score 1685; DB 22; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MRRASRDYTKYLRGSEMGSGPAPHEGPHLHAPPAPHPAPPAASRSMFYALLGLGLGQV 60
Db 1 mrrasrdytkylrgseemggsgpapherplhappppahqpaasrsmfvallg1g1gqv 60
OY 61 VCSVALFFPFAQMDPNRISDGHCTYRILRLHENDFODTTLESODTKLIPSCRRIK 120
Db 61 vcsvalffytgaqmdpnrisedghctylrlrlhenaqfddtlesqdklkipscrrik 120
OY 121 QAFQAVQKELOHTVGSOHTRAEKAMVDGSWDLAKRSKLEAOPFAHLTINATDIPSGSH 180
Db 121 qafqavqkelqhtlvsgshtraekamvsgwldlaksrskleagpfahltinatdipsgsh 180
OY 181 KVSLSWYHDRGWAKISNMFPSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQIMV 240
Db 181 kvs1swyhdrgwakismfngk1iynodgfyllyanlcfrrhetskldateylqimv 240
OY 241 YVTKSTIKIPSSHTLMKGSRTKWSGSEFHPYSINNGFPKLSGGEISTEVSNPSTLD 300
Db 241 yvtks1kipsshtlmkgsrtkwsngsefhpysinngfpklsgeestevsnpstld 300
OY 301 PDODATYFGAFKVRDID 317
Db 301 pdodatyfga1kvridd 317
RESULT 8
AAW83018
ID AAW83018 standard; Protein: 317 AA.
XX AAW83018;
AC AAW83018;
XX 10-FEB-1999 (first entry)
XX Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
KW human.
XX Homo sapiens.
XX OS
XX PN W09846644-A1.
XX PD 22-OCT-1998.
XX PF 15-APR-1998; 98WO-JP01728.
XX PR 02-DEC-1997; 97JP-0332241.
XX PR 15-APR-1997; 97JP-0097808.
XX PR 09-JUN-1997; 97JP-0151434.
XX PR 12-AUG-1997; 97JP-0217897.
XX PR 21-AUG-1997; 97JP-0224803.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX PI Goto M, Higashio K, Kinoshaki M, Kobayashi F, Morinaga T;
PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX MPI: 1998-594563/50.
XX DR N-PSDB: AAV69887.
XX PT Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism

XX S0 Claim 36; Pages 113-114; 151pp; Japanese.
XX PS
XX CC The present sequence represents an osteoclastogenesis inhibitory factor
XX CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
XX CC separation and maturation of osteoclasts in the presence of bone
XX CC absorption factors such as calcitriol or parathyroid hormone (PTH).
XX CC OBM is isolated from stroma cells cultured in the presence of a bone
XX CC absorption factor by separation and solubilisation of membrane proteins
XX CC then affinity chromatography using OCIF. It exists in a full-sequence
XX CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
XX CC used for screening potential inhibitors and modifiers of its biological
XX CC activity, and screening for receptors to OBM which mediate its function.
XX CC These substances can then be used in the treatment of disorders of bone
XX CC function and calcium metabolism. The antibodies can be used for assay
XX CC of the protein, for investigative and diagnostic purposes, and as
XX CC components of drugs.
XX S0 Sequence 317 AA;
Query Match 99.5%; Score 1677; DB 19; Length 317;
Best Local Similarity 99.7%; Pred. No. 1.6e-155;
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MRRASRDYTKYLRGSEMGSGPAPHEGPHLHAPPAPHPAPPAASRSMFYALLGLGLGQV 60
Db 1 mrrasrdytkylrgseemggsgpapherplhappppahqpaasrsmfvallg1g1gqv 60
OY 61 VCSVALFFPFAQMDPNRISDGHCTYRILRLHENDFODTTLESODTKLIPSCRRIK 120
Db 61 vcsvalffytgaqmdpnrisedghctylrlrlhenaqfddtlesqdklkipscrrik 120
OY 121 QAFQAVQKELOHTVGSOHTRAEKAMVDGSWDLAKRSKLEAOPFAHLTINATDIPSGSH 180
Db 121 qafqavqkelqhtlvsgshtraekamvsgwldlaksrskleagpfahltinatdipsgsh 180
OY 181 KVSLSWYHDRGWAKISNMFPSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQIMV 240
Db 181 kvs1swyhdrgwakismfngk1iynodgfyllyanlcfrrhetskldateylqimv 240
OY 241 YVTKSTIKIPSSHTLMKGSRTKWSGSEFHPYSINNGFPKLSGGEISTEVSNPSTLD 300
Db 241 yvtks1kipsshtlmkgsrtkwsngsefhpysinngfpklsgeestevsnpstld 300
OY 301 PDODATYFGAFKVRDID 317
Db 301 pdodatyfga1kvridd 317
RESULT 9
AAW83194
ID AAW83194 standard; Protein: 316 AA.
XX AAW83194;
AC AAW83194;
XX 11-FEB-1999 (first entry)
XX Human osteoprotegerin binding protein from the 32D-F3 ins.
XX Human; osteoprotegerin binding protein; OPB binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODR;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
KW Paget's disease.
XX Homo sapiens.
XX OS
XX PN W09846751-A1.
XX PD 22-OCT-1998.
XX PF 15-APR-1998; 98WO-US07584.
XX

PR 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ.
 DR WPI: 1998-594578/50.
 DR N-PSDB: AAV70284.
 XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 PS
 PS Claim 19; Fig 1; 47pp; English.
 CC The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OC) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 CC
 XX
 XX Sequence 316 AA:
 SQ
 Query Match 84.1%; Score 1417.5; DB 19; Length 316;
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

YY 1 MRASRDYTYRLRGSEEMGGPGAPHEGRLH-APPAPAPQPPAASRSMFVALGLGLQ 59
 DB 1 mrrasrdykyllrseemgsgpyrphgprlhpapsapapppaarsmftallg1g1gq 60
 YY 60 VVCSVALFFFRRAQMDPNRISSEDTGCTIVRLRHENADFDOTTLBSQDTKLIPDSGCRRI 119
 DB 61 vvcsialfllyfraqmdpnrisdscthfyrllrhenagldstlseadct--lpdsctrm 118
 YY 120 KOAFQGAQVOKELQHVGSQHLRAEKAWDGSWDLAKRSKLEQPFALHTLNANDIPSGS 179
 DB 119 kqafgavqkqlqhlvgsqhlfsagapamgswldvagrgrkpeapfahltlnaas1psgs 178
 YY 180 HKVSLSSWYHDRGMAKISNMTFSNGKLIIVQDGFYUANYICFRHHHTSGDLATEYLQLM 239
 DB 179 hkvslsswyhdyrgwaksismtlnsgklrvnqdgfylyanlcfhhtsagsvpcdyqlm 238
 YY 240 VYVYTKITIKIPSSHTLMMKGGSTKWSGNSSEHFYSIVNGGFFKRSSEETISIEVNSPDL 299
 DB 239 vvvvktiklpshtlmmkgsstkwsnssefhfyslvnggffkrlsageetisqynpsll 298
 YY 300 DPODATTYFGAFKVRDID 317
 DB 299 dpoqadatyfgafkvqdid 316
 RESULT 10
 AAM83017
 ID AAM83017 standard; Protein; 316 AA.
 XX

AC AAM83017;
 XX
 DT 10-FEB-1999 (first entry)
 XX
 DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 XX
 XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism.
 XX
 OS Unidentified.
 XX
 PN WO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 DR WPI: 1998-594563/50.
 DR N-PSDB: AAV69886.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PS
 PS Claim 8; Pages 106-108; 151pp; Japanese.
 XX
 CC The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilization of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilized form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 CC
 XX
 XX Sequence 316 AA:
 SQ
 Query Match 84.1%; Score 1417.5; DB 19; Length 316;
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

YY 1 MRASRDYTYRLRGSEEMGGPGAPHEGRLH-APPAPAPQPPAASRSMFVALGLGLQ 59
 DB 1 mrrasrdykyllrseemgsgpyrphgprlhpapsapapppaarsmftallg1g1gq 60
 YY 60 VVCSVALFFFRRAQMDPNRISSEDTGCTIVRLRHENADFDOTTLBSQDTKLIPDSGCRRI 119
 DB 61 vvcsialfllyfraqmdpnrisdscthfyrllrhenagldstlseadct--lpdsctrm 118
 YY 120 KOAFQGAQVOKELQHVGSQHLRAEKAWDGSWDLAKRSKLEQPFALHTLNANDIPSGS 179
 DB 119 kqafgavqkqlqhlvgsqhlfsagapamgswldvagrgrkpeapfahltlnaas1psgs 178
 YY 180 HKVSLSSWYHDRGMAKISNMTFSNGKLIIVQDGFYUANYICFRHHHTSGDLATEYLQLM 239

Db 179 hkvlssewyhndrgwakisnmnlngsklrvngdgyfyllanfcfhetsgsvptdyqlm 238
QY 240 VYVTKTSIKTIPSSHTLMKGGSTKYWSGNSEFHFYSINVGCFKRSGEHSIEVSNPSL 299
Db 239 yvvvktstkikpssnlnkgsstkwnsgnsefhfysinvgffklragselslqvsnp11 298
QY 300 DPDDATYFGAFKVRDID 317
Db 299 dpdgaatyfgafkvqddid 316
RESULT 11
AAW59654
ID AAW59654 standard; Protein: 316 AA.
AC AAW59654;
XX
DT 24-SEP-1998 (first entry)
XX
DE Amino acid sequence of mouse 499E9 protein.
XX
KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
KW antagonist; autoimmune disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
KW acute inflammatory response; antibody; antigen; cancer.
XX
OS Mus sp.
FH
FH Key Location/Qualifiers
FT Domain 1..49 /note= "intracellular domain"
FT Domain 70..316 /note= "extracellular domain"
XX
PN WO9825958-A2.
XX 18-JUN-1998.
XX
PF 12-DEC-1997; 97WO-US22766.
XX
PR 13-DEC-1996; 96US-0032846.
XX (SCHE) SCHERING CORP.
XX
PI Gorman DM, Matson JD;
XX WPI: 1998-348452/30.
DR N-PSDB; AAV41489.
XX
PT Mouse cell surface antigen, 499E9 protein - used to treat conditions
PT associated with abnormal physiology or development
XX
XX Claim 1; Pages 8-11; 59pp; English.
XX
XX This is the amino acid sequence of the mouse 499E9 protein, used
XX in the method of the invention to treat conditions associated with
XX abnormal physiology or development. The 499E9 protein is expressed
XX highly on polarised Th1 T cells, binding of 499E9 to its receptor may
XX result in either immune cell expansion or apoptosis. Antagonists of
XX 499E9 may be used to modulate immune responses in abnormal situations,
XX e.g. autoimmune disorders including rheumatoid arthritis, systemic
XX lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
XX acute inflammatory responses in which T-cell expansion, activation or
XX immunological T-cell memory play an important role. The antibodies
XX can be used to raise anti-idiotypic antibodies which will be useful
XX in detecting or diagnosing various immunological conditions related to
XX the expression of antigens of 499E9. The antibodies, and fragments of
XX 499E9 can be used in the treatment of conditions associated with
XX abnormal physiology or development, including abnormal proliferation
XX (e.g. cancerous conditions) or degenerative conditions.
XX
XX Sequence 316 AA;
SQ

Query Match 84.1%; Score 1417.5; DB 19; Length 316;
Best Local Similarity 84.3%; Pred. No. 3.8e-130;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;
QY 1 MRRASRDYTKYLKSGSEMGGPGAPNHEGPIH-APPAPAPQPPAASRMFVALLGLGQ 59
Db 1 mrrasrdytkylrsgseemsgpgpnhgpphlpapsapapppaasrmfiallg1g19q 60
QY 60 VVCSVALFFTFRAQMDPNKRISDEGTHCIRLRKHEADRDVTLRESQDRLKLPDSQRR 119
Db 61 vvcsialfilyfraqmdpnrisedsthfyrllrhenajldstlesedc--lpsdscrrm 118
QY 120 KOAFQGVOKELHIVGSOHRAEKAMVDSWDLAKRSKLEAPFHLRTNADIPSGS 179
Db 119 kqatfgavqkelqhlvgpqrfgsgapamngswldvqgkpeapghltnaasipsgs 178
QY 180 HKVSLSSWYHDGKWKAKISNMTFSNGKLIYNODGFYLYANICFRHHTSGDLATEYLQLM 239
Db 179 hkvlssewyhndrgwakisnmnlngsklrvngdgyfyllanfcfhetsgsvptdyqlm 238
QY 240 VYVTKTSIKTIPSSHTLMKGGSTKYWSGNSEFHFYSINVGCFKRSGEHSIEVSNPSL 299
Db 239 yvvvktstkikpssnlnkgsstkwnsgnsefhfysinvgffklragselslqvsnp11 298
QY 300 DPDDATYFGAFKVRDID 317
Db 299 dpdgaatyfgafkvqddid 316
RESULT 12
AAV17874
ID AAV17874 standard; Protein: 316 AA.
XX
AC AAV17874;
XX
DT 17-AUG-1999 (first entry)
XX
DE Murine TRANCE.
XX
KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
KW TNF-related activation induced cytokine; immune response; cancer;
KW autoimmune disease; HIV; hypersensitivity; allergen.
XX
OS Mus musculus.
XX
FN WO9929865-A2.
XX
PD 17-JUN-1999.
XX
PF 14-DEC-1998; 98WO-US26486.
XX
PR 11-DEC-1998; 98US-0989479.
PR 12-DEC-1997; 97US-0989479.
PR 03-MAR-1998; 98US-0034099.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Choi Y, Josien R, Steinman R, Won B;
XX WPI: 1999-385609/32.
DR N-PSDB; AAX80224.
XX
XX TNF like proteins for treating autoimmunity and cancer
XX
XX Claim 9; Fig 3; 164pp; English.
XX
XX The present sequence represents murine TNF-related activation induced
XX cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX variants, fragments, derivatives or analogues may be used as modulators
XX of immune response in a mammal comprising human and/or murine TRANCE.
XX
XX TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX

| FT | Domain | 152..316 | /note="tumour necrosis factor-like domain" |
|----|---|--|--|
| FT | Region | 158..317 | /note="active ligand moiety" |
| XX | PN | WO200015807-A1. | |
| XX | PD | 23-MAR-2000. | |
| XX | PF | 13-SEP-1999; | 99WO-DK00481. |
| XX | PR | 15-SEP-1998; | 98DK-0001164. |
| XX | PR | 02-OCT-1998; | 98US-0102896. |
| PA | (MEBT-) M & E BIOTECH AS. | | |
| XX | PI | Halkier T, Haaning J; | |
| XX | PI | WPI: 2000-271444/23. | |
| DR | N-PSDB; AAZ99965. | | |
| PT | In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis - | | |
| PS | Claim 17; Page 81-82; 110pp; English. | | |
| CC | The present sequence represents a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption. | | |
| XX | Sequence | 316 AA: | |
| SO | Query Match | 84.1%; Score 1417.5; DB 21; Length 316; | |
| | Best Local Similarity | 84.3%; Pred. No. 3.8e-130; | |
| | Matches | 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2; | |
| OY | 1 | MRRARDDTKYIRGSEEMGGCGARHHEGPLH-APPAPAHOPAPASRSMFVALLGIGLQ | 59 |
| DB | 1 | | 60 |
| | 1 | mtaraadgkykylrseemgsgpvgvhegplhpapapapappapapastsmflaligligq | 60 |
| OY | 60 | VCSVALFFYFRAQMDPNRISDEGTHCYRIILRLHENADFQDTLESQDTKLIPDSCRRI | 119 |
| OY | 60 | | 119 |
| DB | 61 | vvcsialflfytraqmdpnrisdeschcfryllrlrhenagldgstleset--lpdsctrm | 118 |
| OY | 120 | KQAFGAVQKELQHVGSCHIRAEKAMVDGSLDLAKSKLEAQPPAHLTINATIDIPSS | 179 |
| DB | 119 | kgafgavqkqlqhvtpqrfisgapamnegswldvaqirgkpeaqpfahltlnaasipsgs | 178 |
| OY | 180 | HKVSSSNVHHDGMAKISMFTSNGKLIYNQGGFYLYLVANICEFRHNETSGDATERIOLM | 239 |
| DB | 179 | hkvtlssvnyhdgvakismftlsmgklyvngdgyfyylyanlcfirhnetsgsvptdylqim | 238 |
| OY | 240 | VYVTKTSIKRIPSSHTLMKGSSTKYWSGNSSEHFHSINVGPFKLSGEEISIEVSNPSSL | 299 |
| DB | 239 | yvvvtsikripsshtlmkgstskwsgnssehfifyslnvgffkrlaageisivqsnpsll | 298 |
| OY | 300 | DPDDATATFGAKRVDDID | 317 |
| DB | 299 | dpddatatyfgalkvqdid | 316 |

| | |
|--|--|
| RESULT | 15 |
| ID | AAY84419 |
| XX | AAI84419 standard; Protein: 316 AA. |
| AC | |
| XX | AAI84419; |
| DT | 25-JUL-2000 (first entry) |
| XX | |
| DE | Amino acid sequence of a murine osteoprotegerin ligand (OPGL). |
| XX | |
| KW | Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; |
| KM | tumour necrosis factor receptor; type II transmembrane protein; |
| KW | osteoclast differentiation; CSF-1; osteoclast activator; |
| KM | immune response; osteoporosis; bone resorption. |
| XX | |
| OS | Mus musculus. |
| XX | |
| FH | Key |
| FT | Region |
| FT | /note= "Location/Qualifiers 49..69 |
| FT | /note= "transmembrane region" |
| FT | Domain |
| FT | /note= "70..157 extracellular stalk domain" |
| FT | Region |
| FT | /note= "158..317 active ligand moiety" |
| XX | |
| PN | WO20015807-A1. |
| XX | |
| PD | 23-MAR-2000. |
| XX | |
| PF | 13-SEP-1999; 99WO-DK00481. |
| XX | |
| PR | 15-SEP-1998; 98DK-0001164. |
| PR | 02-OCT-1998; 98US-0102896. |
| XX | |
| PA | (MEBI-) M & E BIOTECH AS. |
| XX | |
| PI | Halkier T, Haaning J; |
| XX | |
| DR | WI: 2000-271444/23. |
| DR | N-PSDB; AAZ99966. |
| XX | |
| PT | In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis - |
| XX | |
| PS | Claim 17; Page 85-86; 110pp; English. |
| XX | |
| CC | The present sequence represents a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption. |
| XX | |
| SQ | Sequence 316 AA: |
| Query Match | 84.1%; Score 1417.5; DB 21; Length 316; |
| Best Local Similarity | 84.3%; Pred. No. 3.8e-130; |
| Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2; | |
| QY | 1 MRRASRDYTKYLGRGSEMGCGAPHEGPLH-APPPPAPHOPPAASRSMTVALIGLGIQ 59 |
| Db | 1 mrrasrdytkylrsgseemgspgyphgeplhpapapapappapaasmfiallglygq 60 |
| QY | 60 VCVSAVFPEFRAMDPNRISEDGHICITRILRLHENADFDOTLESODTKLIIPDSCRI 119 |

```

Db 61 vvcsialfleyfraqmdparlisedstchcfyrlrlhenagldstlesedc--lpdscrm 118
OY 120 KOAFQGAIVQKELQHIIVGSOHRAEKAWVDGSMDLAKRSKLEAOPFAHLTINATDIPSGS 179
Db 119 kga fga vqkelqnlvppqrfsgapammegswldvaqrgkpeaqpfahltinaaslpsgs 178
OY 180 HKVSLSSWYHNRGNAKISNMTFSNGKLIYNODGFYLYANICFRHHETSGLATEYLQIM 239
Db 179 hkvlsawyhdtgwkakismclsnqklrvngdfylyanlcfthetsgsvptdyqlm 238
OY 240 VYVTKTSIKIPSSHTLKMGGSTKTYWGSNEFHFYSINVGFFKLRSGEISIEVSNPSLL 299
Db 239 vvvvktstklpsshlmkgscknwsngnefhyfsinvgffklragselisyvsnpsll 298
OY 300 DPDDATYEGAFKVRDID 317
Db 299 dpdgdalyfgafkvqdda 316

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Search completed: July 8, 2002, 20:05:55
 Job time: 699 sec

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: July 8, 2002, 20:01:06 ; Search time 52.39 Seconds
(without alignments)
147.794 Million cell updates/sec

Title: US-09-865-363-13

Perfect score: 1685

Sequence: 1 MRRASRDYTKYLGRSEMGCG.....LDDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1685 | 100.0 | 317 | 3 | US-08-996-139-13 |
| 2 | 1685 | 100.0 | 317 | 4 | US-08-995-659-13 |
| 3 | 1685 | 100.0 | 317 | 4 | US-09-215-649A-13 |
| 4 | 1685 | 100.0 | 317 | 4 | US-09-052-521C-4 |
| 5 | 1417.5 | 84.1 | 316 | 2 | US-08-842-842-7 |
| 6 | 1417.5 | 84.1 | 316 | 4 | US-08-989-362-2 |
| 7 | 1417.5 | 84.1 | 316 | 4 | US-09-052-521C-2 |
| 8 | 1336.5 | 78.7 | 294 | 3 | US-08-996-139-11 |
| 9 | 1336.5 | 78.7 | 294 | 4 | US-08-995-659-11 |
| 10 | 1336.5 | 78.7 | 294 | 4 | US-09-215-649A-11 |
| 11 | 251.5 | 14.9 | 279 | 4 | US-09-072-993C-3 |
| 12 | 251.5 | 14.9 | 281 | 4 | US-08-670-354-2 |
| 13 | 251.5 | 14.9 | 281 | 3 | US-08-584-031-1 |
| 14 | 251.5 | 14.9 | 281 | 3 | US-08-780-496-1 |
| 15 | 251.5 | 14.9 | 281 | 4 | US-08-883-086-10 |
| 16 | 251.5 | 14.9 | 281 | 4 | US-09-320-424-2 |
| 17 | 251.5 | 14.9 | 281 | 4 | US-09-333-593A-6 |
| 18 | 251.5 | 14.9 | 281 | 4 | US-09-320-424-11 |
| 19 | 248 | 14.7 | 291 | 1 | PCT-US96-10895-2 |
| 20 | 248 | 14.7 | 291 | 1 | PCT-US96-10895-6 |
| 21 | 248 | 14.7 | 291 | 5 | PCT-US96-10895-6 |
| 22 | 236.5 | 14.0 | 253 | 4 | US-09-320-424-11 |
| 23 | 236.5 | 14.0 | 253 | 4 | US-09-320-424-11 |
| 24 | 231.5 | 13.7 | 177 | 4 | US-09-105-343A-7 |
| 25 | 226.5 | 13.4 | 183 | 4 | US-09-105-343A-8 |
| 26 | 189 | 11.2 | 281 | 4 | US-08-810-453-2 |
| 27 | 189 | 11.2 | 281 | 3 | US-08-815-190A-2 |

| | | | | | | |
|----|-------|------|-----|---|------------------|-------------------|
| 28 | 189 | 11.2 | 281 | 4 | US-09-290-640-25 | Sequence 25, Appl |
| 29 | 189 | 11.2 | 281 | 4 | US-09-479-524-3 | Sequence 3, Appl |
| 30 | 189 | 11.2 | 281 | 4 | US-08-339-214-8 | Sequence 8, Appl |
| 31 | 189 | 11.2 | 281 | 4 | US-08-339-214-30 | Sequence 30, Appl |
| 32 | 189 | 11.2 | 281 | 5 | PCT-US95-00362-2 | Sequence 2, Appl |
| 33 | 184.5 | 10.9 | 279 | 4 | US-08-339-214-24 | Sequence 24, Appl |
| 34 | 184.5 | 10.9 | 279 | 4 | US-08-339-214-32 | Sequence 32, Appl |
| 35 | 184.5 | 10.9 | 279 | 5 | PCT-US95-00362-5 | Sequence 5, Appl |
| 36 | 175.5 | 10.4 | 278 | 4 | US-08-339-214-16 | Sequence 16, Appl |
| 37 | 175.5 | 10.4 | 278 | 4 | US-08-339-214-26 | Sequence 26, Appl |
| 38 | 164.5 | 9.8 | 376 | 3 | US-08-751-512-8 | Sequence 8, Appl |
| 39 | 158.5 | 9.4 | 261 | 1 | US-07-940-605A-2 | Sequence 2, Appl |
| 40 | 158.5 | 9.4 | 261 | 1 | US-08-184-422-8 | Sequence 8, Appl |
| 41 | 158.5 | 9.4 | 261 | 1 | US-08-360-823A-2 | Sequence 2, Appl |
| 42 | 158.5 | 9.4 | 261 | 1 | US-08-446-822-4 | Sequence 4, Appl |
| 43 | 158.5 | 9.4 | 261 | 2 | US-08-431-055-4 | Sequence 4, Appl |
| 44 | 158.5 | 9.4 | 261 | 2 | US-08-690-096-2 | Sequence 2, Appl |
| 45 | 158.5 | 9.4 | 261 | 2 | US-08-249-189-12 | Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13


```

? ATTORNEY/AGENT INFORMATION:
? NAME: Perkins, Patricia Anne
? REGISTRATION NUMBER: 34,693
? REFERENCE/DOCKET NUMBER: 2851-P-
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206)587-0430
? TELEFAX: (206)233-0644
? INFORMATION FOR SEQ ID NO: 13:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 317 amino acids
?
? TYPE: amino acid
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

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| | | | | |
|---------------------------|--------|---------------------|------|-------------|
| Query Match | 100.0% | Score 1685: | DB 4 | Length 317; |
| Best Local Similarity | 100.0% | Pred. No. 9.8e-164; | | |
| Matches 317; Conservative | 0; | Mismatches | 0; | Gaps 0; |

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|----|-----|---|-----|
| QY | 1 | MRRASRDYTKYLRGSEEGGCGPAPNHSGRPLAAPPAPAPORPARASRMFAALLGLGIGQV | 60 |
| Db | 1 | MRRASRDYTKYLRGSEEGGCGPAPNHSGRPLAAPPAPAPORPARASRMFAALLGLGIGQV | 60 |
| QY | 61 | VCSSALFFYFAQMDPNRISDGTNCTIYRILRLHENDFODTLESODTKLIPDSCKRIK | 120 |
| Db | 61 | VCSSALFFYFAQMDPNRISDGTNCTIYRILRLHENDFODTLESODTKLIPDSCKRIK | 120 |
| QY | 121 | QAFQGAQVQKELQHTVGSQHIIEAKAMVDGSMILDAKRSKLEAPCFALITINATDIPSGSH | 180 |
| Db | 121 | QAFQGAQVQKELQHTVGSQHIIEAKAMVDGSMILDAKRSKLEAPCFALITINATDIPSGSH | 180 |
| QY | 181 | KVSISSSWYHDHGMAKKISNMFSSNCKLLVNDGFTYLLYANICFRHNHETSGDLATEYLOLMV | 240 |
| Db | 181 | KVSISSSWYHDHGMAKKISNMFSSNCKLLVNDGFTYLLYANICFRHNHETSGDLATEYLOLMV | 240 |
| QY | 241 | YVTKTSIKIPSSSHLLMKGGSTKYWGSNSEHFHYISINVGGFFKLRSGEIISLEVSNPSLLD | 300 |
| Db | 241 | YVTKTSIKIPSSSHLLMKGGSTKYWGSNSEHFHYISINVGGFFKLRSGEIISLEVSNPSLLD | 300 |
| QY | 301 | PDQDATYFGAKRVADID 317 | |
| Db | 301 | PDQDATYFGAKRVADID 317 | |

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RESULT 4
US-09-052-521C-4
: Sequence 4, Application US/09052521C
: Patent No. 6316408
: GENERAL INFORMATION:
: APPLICANT: Boyle, William J.
: TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
: FILE REFERENCE: A-4518rv
: CURRENT APPLICATION NUMBER: US/09/052,521C
: CURRENT FILING DATE: 1998-03-30
: PRIOR APPLICATION NUMBER: 08/880,855
: PRIOR FILING DATE: 1997-06-23
: PRIOR APPLICATION NUMBER: 08/842,842
: PRIOR FILING DATE: 1997-04-16
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 317
: TYPE: PRT
: ORGANISM: Human
: US-09-052-521C-4

```

| | | | | |
|-----------------------|----------------|--------------|----------|------------|
| Query Match | 100.0% | Score 1685 | DB 4 | Length 317 |
| Best Local Similarity | 100.0% | Pred. No. 9 | 8e-16 | |
| Matches 317 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

[illegible]

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1      RESULT 5
2      US-08-842-842-7
3      ; Sequence 7, Application US/08842842
4      ; Patent No. 5843678
5      ;
6      GENERAL INFORMATION:
7      APPLICANT: Boyle, William J.
8      TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
9      NUMBER OF SEQUENCES: 7
10     CORRESPONDENCE ADDRESSES:
11     ADDRESSEE: Amgen Inc.
12     STREET: 1840 Dehavilland Drive
13     CITY: Thousand Oaks
14     STATE: California
15     COUNTRY: USA
16     ZIP: 91230-1789
17
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: PatentIn Release #1.0, Version #1.30
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/842,842
25     FILING DATE:
26     CLASSIFICATION: 435
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Winter, Robert B.
29     REFERENCE/DOCKET NUMBER: A-451
30     INFORMATION FOR SEQ ID NO: 1:
31     SEQUENCE CHARACTERISTICS:
32     LENGTH: 316 amino acids
33     TYPE: amino acid
34     TOPOLOGY: linear
35     MOLECULE TYPE: protein
36     US-08-842-842-7

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| | | | | |
|-----------------------|-----------------|--------------------|----------|------------|
| Query Match | 84.1% | Score 1417.5 | DB 2 | Length 316 |
| Best Local Similarity | 84.3% | Pred. No. 1.9e-136 | | |
| Matches 268 | Conservative 16 | Mismatches 31 | Indels 3 | Gaps 2 |

| | | | |
|----|----|--|-----|
| QY | 1 | MRRAASRDVTKTLRSEEGGGGPGAPHEGCPHL-APPAPAPHPAPAAASMSMVALLLGLG | 59 |
| Db | 1 | MRRAASRDVTKTLRSEEGGGGPGAPHEGCPHL-APPAPAPHPAPAAASMSMVALLLGLG | 60 |
| QY | 60 | VVCSVALFEFFFRRAADMPNRISSEDGTHCIYRIIRLHENADFDOTTLLESQDKLLPDSCRI | 119 |
| Db | 61 | VVCSIALELFEFRRAADMPNRISSEDGTHCFYILRIHENAGLQDSTLEEDT--LPDSCRR | 118 |

| | | | |
|----|-----|--|-----|
| Qy | 120 | KOAFQAVOKELHITVSSONHRAKAWDSSWIDLARSKLEOPFHLITNTDIPSGS | 179 |
| Db | 119 | KOAFQAVOKELHITVBPQFSCSAPAMBSWIDLVAQRCRPEAOFRPHLITNAPSISGS | 178 |
| Qy | 180 | HKVSLSWYHDRCMAKTSNMFTNSGKLTIVNODGFYLYLANICFRNHETSGDLATEYLQIM | 239 |
| Db | 179 | HKVLLSWYHDRCMAKTSNMFTLSNGKLRVNODGFYLYLANICFRNHETSGSVPLDYQLM | 238 |
| Qy | 240 | VYVYKTSIKIPSSMTLMKGSSTKWSGNSNPHFSLINVGGRPFKRSGEELISIEVNSPIL | 299 |
| Db | 239 | VYVYKTSIKIPSSNMLMKGSGTKMWSGNSNPHFSLINVGGEFLKRGEEELISIOVNSPIL | 298 |
| Qy | 300 | DPDODATFYGAFKVRDID | 317 |
| Db | 299 | DPDODATFYGAFKYQDID | 316 |

RESULT 6
US-08-989-362-2
; Sequence 2, Application US/08989362
Patent No. 634586

```

1  GENERAL INFORMATION:
2  APPLICANT: Gorman, Daniel M.
3  APPLICANT: Mattson, Jeanine D.
4  TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
5  TITLE OF INVENTION: Reagents
6  NUMBER OF SEQUENCES: 2
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: DNAX Research Institute
9  STREET: 901 California Avenue
10 CITY: Palo Alto
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94304-1104
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/989,362
21 FILING DATE: 12-DEC-1997
22 CLASSIFICATION: 56
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 60/032,846
25 FILING DATE: 13-DEC-1996
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Ching, Edwin P.
28 REGISTRATION NUMBER: 34,090
29 REFERENCE/DOCKET NUMBER: DX0686
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (650)852-9196
32 TELEFAX: (650)496-1204
33 INFORMATION FOR SEQ ID NO: 2:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 316 amino acids
36 TYPE: amino acid
37 TOPOLOGY: linear
38 MOLECULE TYPE: protein
39
40 US-08-989-362-2

```

| | | | | | | | | | |
|-----------------------|-------|--------------|--------------|------------|--------|--------|---|------|---|
| Query Match | 84.1% | Score | 1417.5 | DB 4 | Length | 316 | | | |
| Best Local Similarity | 84.3% | Pred | No. 1.9e-136 | | | | | | |
| Matches | 268 | Conservative | 16 | Mismatches | 31 | Indels | 3 | Gaps | 2 |

QY 1 MRRASRDTYKTLRSGEEMGGSPGAPHPHCPLH - APPAPPHQPPAASMSMVALLLGLGQ 59
Db 1 MRRASRDQGTKLIRSGEESGSGVPHPEPLPAPASAPAPPPAASMSMVALLLGLGQ 60
QY 60 VVCSVALFFYPPAAMDPRISIEDGCTGCTYLRLLRHENNAODITLLESDQTKLPIDSCRAI 119
Db 61 VVCSIALFLYPPAAMDPRISIEDGCTGCTYLRLLRHENNAODITLLESDT - LPDSCRM 118

[illegible]

RESULT 7
US-09-052-521C-2
; Sequence 2, Application US/09052521C

```

1  GENERAL INFORMATION:
2  APPLICANT: Boyle, William J.
3  TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
4  FILE REFERENCE: A-451BIV
5  CURRENT APPLICATION NUMBER: US/09/052,521C
6  CURRENT FILING DATE: 1998-03-30
7  PRIOR APPLICATION NUMBER: 08/880,855
8  PRIOR FILING DATE: 1997-06-23
9  PRIOR APPLICATION NUMBER: 08/842,842
10 PRIOR FILING DATE: 1997-04-16
11 NUMBER OF SEQ ID NOS: 40
12 SOFTWARE: PatentIn Ver. 2.1
13 SEQ ID NO 2
14 LENGTH: 316
15 TYPE: PRT
16 ORGANISM: Mouse
17 US-09-052-521C-2

```

| | | | | |
|-----------------------|-----------------|--------------------|----------|------------|
| Query Match | 84.1% | Score 1417.5 | DB 4 | Length 316 |
| Best Local Similarity | 84.3% | Match No. 1.9e-136 | | |
| Matches 268 | Conservative 16 | Mismatches 31 | Indels 3 | Gaps 2 |

| | | | |
|----|-----|--|-----|
| Qy | 1 | MRRASRQYTKLRSESEMGSGDPADPHGCPRLH-APPAPADPHQASMSMVALLGGLGQ | 59 |
| Db | 1 | MRRASRSDGKTLRSESEMGSGDPVPHGCPRLHAPASADAPAPPAASKSMFLALGLGGLGQ | 60 |
| Qy | 60 | VYCSALFEYFRAMDMPRISEDSTHCTIYRLRLRHENADQODTTLSEQDRLKLPDSCRI | 119 |
| Db | 61 | VYCSIALFLYLRAMDMPRISEDSSTHCFYRLRLRHENAGLQDSTLSESDI--LPDSCRIM | 118 |
| Qy | 120 | KQAFQGAQVQKELQHLIVGSOHLRAEKAVYDGSWLDLAKRSKLEQAFALHTITMATDIPGS | 179 |
| Db | 119 | KQAFQGAQVQKELQHLIVGQRFRESGAPAMMGESWLDVAQRGKEADQFALHTITMAISIPGS | 178 |
| Qy | 180 | HKVELSSWYHHRGNAKISNMFTFSNGKLLVNDGGYYLLANTCFPHHETSDGLAEVYQLM | 239 |
| Db | 179 | HKVELSSWYHHRGNAKISNMFTLSNGKLRVNDGGYYLLANCFPHHETSGSVPPDYQLM | 238 |
| Qy | 240 | VYVTKTSIKTIPSSHTLMKGSTKQWMSGSEPHFYSINVGGFPRKSRSEIISIEVSNPDL | 299 |
| Db | 239 | VYVTKTSIKTIPSSHMLMGSGSTKQWMSGSEPHFYSINVGGFPRKLRAGDEIISIQVSNPDL | 298 |
| Qy | 300 | DPDQDATYFGAFKRYDID | 317 |
| Db | 299 | DPDQDATYFGAFKYODID | 316 |

RESULT 8
US-08-996-139-11
; Sequence 11, Application US/08996139


```
Patent No. 6017729
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/996,139
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US95N 60/064,671
: FILING DATE: 14 OCTOBER 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-996-139-11
```

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Query Match 78.7%; Score 1326.5; DB 3; Length 294;
Best Local Similarity 84.5%; Pred. No. 3.2e-127;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

QY 23 GAPHEGPLH-APPAPHPAPPAASRSMFVALLGLGLOVGVCSVALFFFRQMDPNRISE 81
DB 1 GVPHGEPHLPAPAPAPAPPAASRSMFVALLGLGLOVGVCSVALFFFRQMDPNRISE 60
QY 82 DGTICIRILRLHFNADFDOTLTLESQDTKLIPDSCRIRKQAFQAVQKELQHYVGSQHIR 141
DB 61 DSTHCFRILRLHFNADFDOTLTLESQDTKLIPDSCRIRKQAFQAVQKELQHYVGSQHIR 118
QY 142 AEKAMVDGSMIDLAKRSLKLEQAPFAHLITINATDIPSGSHKVSLSWYHNRGMKISNMTF 201
DB 119 GAPAMMGSMIDLAKRSLKLEQAPFAHLITINATDIPSGSHKVSLSWYHNRGMKISNMTL 178
QY 202 SNGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPSSHLMKGGST 261
DB 179 SNGKLIYNODGFYLLYANICFRHHETSGSVPTDYLQMLVYVTKTSIKIPSSHLMKGGST 238
QY 262 KYNSGNSFHHYTSINNGCFKLSGSESTIVSNPSLDPPQDATYTGAFKRVRID 317
DB 239 KNSGNSFHHYTSINNGCFKLSGSESTIVSNPSLDPPQDATYTGAFKRVRID 294
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RESULT 9
US-08-995-659-11
: Sequence 11, Application US/08995659
: Patent No. 6242213
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/995,659
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US95N 60/064,671
: FILING DATE: 14 OCTOBER 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-995-659-11
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Query Match 78.7%; Score 1326.5; DB 4; Length 294;
Best Local Similarity 84.5%; Pred. No. 3.2e-127;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

QY 23 GAPHEGPLH-APPAPHPAPPAASRSMFVALLGLGLOVGVCSVALFFFRQMDPNRISE 81
DB 1 GVPHGEPHLPAPAPAPAPPAASRSMFVALLGLGLOVGVCSVALFFFRQMDPNRISE 60
QY 82 DGTICIRILRLHFNADFDOTLTLESQDTKLIPDSCRIRKQAFQAVQKELQHYVGSQHIR 141
DB 61 DSTHCFRILRLHFNADFDOTLTLESQDTKLIPDSCRIRKQAFQAVQKELQHYVGSQHIR 118
QY 142 AEKAMVDGSMIDLAKRSLKLEQAPFAHLITINATDIPSGSHKVSLSWYHNRGMKISNMTF 201
DB 119 GAPAMMGSMIDLAKRSLKLEQAPFAHLITINATDIPSGSHKVSLSWYHNRGMKISNMTL 178
QY 202 SNGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPSSHLMKGGST 261
DB 179 SNGKLIYNODGFYLLYANICFRHHETSGSVPTDYLQMLVYVTKTSIKIPSSHLMKGGST 238
```



```
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-2

Query Match      14.9%  Score 251.5; DB 1; Length 281;
Best Local Similarity 24.1%  Pred. No. 1.4e-17;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY 42 PAASRMFVALGLGQVCSVALFFYFRAOMD--PRLSEDTGHCYRILRLHENDF 99
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 10 PSLGTCVLIVFYVLLQSLCAVATYYFTNELKQMDKYSKSIAC-----LKED--- 61
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 100 QDTLESODTLIPDSRRITQAFQAVOKELQIHVGSQHIRAEKAWDGSMDLAKRSK 159
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 62 -DSYWDPNDESMNSPCQVQKW-----OLRLVYRKMLRLTSEETI-----STVQEKQ 107
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 160 LEAOPF-----AHLT-----INATDIPSGSHKYSL-----SSWYHDR-GNAKISNM 199
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 108 QNISPLVNERGPQVAAHITGTGRSNTLSSPNSKNEKALGRKINSWSSRSGHSFLSNL 167
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 200 TFSNGKLIVNODGFYVLANICFRHNETSGDLATEYLQLMVYVTKTSIKIPSSHTLKKGG 259
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 168 HLRNGELVYHEKGFYIYSQYFRFQOEIKENTKNDKQMOYIYKYT-SYDPDILLAKSA 226
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 260 STKYWSGSEHFHFYSINVGFFKLRSGEETISEVSNPSLDDPDADATYFGAFKY 313
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 227 RNSCMSKDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
   | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 13
US-08-584-031-1
Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 Ligand
FILE REFERENCE: 11669, 22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
```

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1

Query Match      14.9%  Score 251.5; DB 3; Length 281;
Best Local Similarity 24.1%  Pred. No. 1.4e-17;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY 42 PAASRMFVALGLGQVCSVALFFYFRAOMD--PRLSEDTGHCYRILRLHENDF 99
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 10 PSLGTCVLIVFYVLLQSLCAVATYYFTNELKQMDKYSKSIAC-----LKED--- 61
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 100 QDTLESODTLIPDSRRITQAFQAVOKELQIHVGSQHIRAEKAWDGSMDLAKRSK 159
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 62 -DSYWDPNDESMNSPCQVQKW-----OLRLVYRKMLRLTSEETI-----STVQEKQ 107
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 160 LEAOPF-----AHLT-----INATDIPSGSHKYSL-----SSWYHDR-GNAKISNM 199
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 108 QNISPLVNERGPQVAAHITGTGRSNTLSSPNSKNEKALGRKINSWSSRSGHSFLSNL 167
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 200 TFSNGKLIVNODGFYVLANICFRHNETSGDLATEYLQLMVYVTKTSIKIPSSHTLKKGG 259
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 168 HLRNGELVYHEKGFYIYSQYFRFQOEIKENTKNDKQMOYIYKYT-SYDPDILLAKSA 226
   | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 260 STKYWSGSEHFHFYSINVGFFKLRSGEETISEVSNPSLDDPDADATYFGAFKY 313
   | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 227 RNSCMSKDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
   | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 14
US-08-780-496-1
Sequence 1, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntcharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinpatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-780-496-1
```


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THIS PAGE BLANK (USPTO)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 8, 2002, 18:51:49 ; Search time 52.04 Seconds

(without alignments)
235.859 Million cell updates/sec

Title: US-09-865-363-13

Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEMG.....LDDPDADTYFGAFYKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwIsprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1685 | 100.0 | 317 | 1 | TN11_HUMAN |
| 2 | 1417.5 | 84.1 | 316 | 1 | TN11_MOUSE |
| 3 | 251.5 | 14.9 | 281 | 1 | TN10_MOUSE |
| 4 | 248 | 14.7 | 291 | 1 | TN10_MOUSE |
| 5 | 189 | 11.2 | 281 | 1 | FASL_HUMAN |
| 6 | 184.5 | 10.9 | 279 | 1 | FASL_MOUSE |
| 7 | 176.5 | 10.5 | 261 | 1 | TNFS_BOVIN |
| 8 | 175.5 | 10.4 | 278 | 1 | FASL_RAT |
| 9 | 158.5 | 9.4 | 261 | 1 | TNFS_HUMAN |
| 10 | 152 | 9.0 | 260 | 1 | TNFS_FELCA |
| 11 | 146 | 8.7 | 234 | 1 | TNFA_CAVPO |
| 12 | 145 | 8.6 | 260 | 1 | TNFS_CAVPO |
| 13 | 141.5 | 8.4 | 235 | 1 | TNFA_MOUSE |
| 14 | 140.5 | 8.3 | 235 | 1 | TNFA_RABIT |
| 15 | 137 | 8.1 | 234 | 1 | TNFA_SHEEP |
| 16 | 134 | 8.0 | 233 | 1 | TNFA_MACFA |
| 17 | 134 | 8.0 | 230 | 1 | TN14_HUMAN |
| 18 | 133 | 7.9 | 233 | 1 | TNFA_HUMAN |
| 19 | 133 | 7.9 | 233 | 1 | TNFA_CANFA |
| 20 | 133 | 7.9 | 233 | 1 | TNFA_MOUSE |
| 21 | 132.5 | 7.9 | 233 | 1 | TNFA_HUMAN |
| 22 | 131.5 | 7.8 | 235 | 1 | TNFA_PERLE |
| 23 | 130.5 | 7.7 | 235 | 1 | TNFA_RAT |
| 24 | 130 | 7.7 | 306 | 1 | TNFC_MOUSE |
| 25 | 129.5 | 7.7 | 233 | 1 | TNFA_PAPSP |
| 26 | 129 | 7.6 | 233 | 1 | TNFA_MARMO |
| 27 | 129 | 7.6 | 234 | 1 | TNFA_PAPHU |
| 28 | 126.5 | 7.5 | 233 | 1 | TNFA_HORSE |
| 29 | 126 | 7.5 | 232 | 1 | TNFA_BOVIN |
| 30 | 122 | 7.2 | 133 | 1 | TNFA_PIG |
| 31 | 120 | 7.1 | 133 | 1 | TNFA_CAVHI |
| 32 | 118 | 7.0 | 229 | 1 | TNFA_CEREL |
| 33 | 117 | 6.9 | 233 | 1 | TNFS_MOUSE |
| | | | | | TNFA_FELCA |

| | | | | | | |
|----|------|-----|------|---|------------|--------------------|
| 34 | 117 | 6.9 | 244 | 1 | TNFC_HUMAN | 00643 homo sapien |
| 35 | 116 | 6.9 | 233 | 1 | TNFA_MACEU | 07764 macropus eu |
| 36 | 105 | 6.2 | 201 | 1 | TNFB_MACEU | 09448 macropus eu |
| 37 | 97 | 5.8 | 1464 | 1 | CALL_HUMAN | P02452 homo sapien |
| 38 | 95 | 5.6 | 858 | 1 | V2A_CMVK | 08673 cucumbe: mo |
| 39 | 93 | 5.5 | 233 | 1 | TNFA_TRIUV | P79374 trichosurus |
| 40 | 92.5 | 5.5 | 205 | 1 | TNFB_HUMAN | P01374 homo sapien |
| 41 | 92.5 | 5.5 | 450 | 1 | YK22_YEAST | P36135 saccharomyc |
| 42 | 92 | 5.5 | 857 | 1 | V2A_CMVNT | 040977 cucumbe: mo |
| 43 | 90.5 | 5.4 | 858 | 1 | V2A_CMVNS | 039436 cucumbe: mo |
| 44 | 90.5 | 5.4 | 1694 | 1 | SN_MOUSE | 062230 mus musculu |
| 45 | 90 | 5.3 | 1460 | 1 | CALL_CANFA | 09x57 canis fam11 |

ALIGNMENTS

| RESULT | ID | TN11_HUMAN | STANDARD: | PRT: | 317 AA. |
|--------|---|-----------------------------------|-----------|------|---------|
| AC | 014788 | 014723; Q9P203; | | | |
| DT | 16-OCT-2001 | (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 | (Rel. 40, Last sequence update) | | | |
| DT | 16-OCT-2001 | (Rel. 40, Last annotation update) | | | |
| DE | Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF). | | | | |
| GN | TNFSF11 OR RANKL OR TRANCE OR OPGL. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| OX | NCBI_Taxid=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=bone marrow, and peripheral blood; | | | | |
| RX | MEDLINE=98032977; PubMed=9367155; | | | | |
| RA | Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.; | | | | |
| RT | "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function."; | | | | |
| RL | Nature 390:175-179(1997). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Lymph node; | | | | |
| RX | MEDLINE=98227661; PubMed=9568710; | | | | |
| RA | Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.; | | | | |
| RT | "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."; | | | | |
| RL | Cell 93:165-176(1998). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE OF 73-317 FROM N.A. | | | | |
| RC | TISSUE=Thymocytes; | | | | |
| RX | MEDLINE=97460112; PubMed=9312132; | | | | |
| RA | Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kladachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.; | | | | |
| RT | "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."; | | | | |
| RL | J. Biol. Chem. 272:25190-25194(1997). | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 2). | | | | |
| RC | TISSUE=Thymocyte; | | | | |
| RX | MEDLINE=20175237; PubMed=10708588; | | | | |
| RA | Nagai M., Kyakumoto S., Sato N.; | | | | |
| RT | "Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation."; | | | | |

```

RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
CC AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
CC HYPERCALCEMIA OF MALIGNANCY
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
CC SECRETED (ISOFORM 2).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/SODF; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NOSES BUT
CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF019047; AAB86811.1; -
DR EMBL: AF053712; AAC39731.1; -
DR EMBL: AF013171; AAC51762.1; -
DR EMBL: AB037599; BAA90488.1; -
DR MIM: 602642; -
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00228; TNF_1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; FALSE_NEG.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor; Alternative splicing
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT POTENTIAL 69 317 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 73 MISSING (IN ISOFORM 2).
FT CONFLICT 194 194 A -> G (IN REF. 3).
SO SEQUENCE 317 AA; 35478 MW; 766176446348097f CRC64;

Query Match 100.0%; Score 1685; DB 1; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.4e-136; Indels 0; Gaps - 0;
Matches 317; Conservative 0; Mismatches 0;

OY 1 MRRASRDYTKYLRGSEEMGGGAPHEGPLAPPPAPHPAPPAASRSFVALGLGLGOV 60
DB 1 MRRASRDYTKYLRGSEEMGGGAPHEGPLAPPPAPHPAPPAASRSFVALGLGLGOV 60
OY 61 VCSVALFFYFRAQMDPNRISDEGTHCIYRIILHLENADFDTTLESQDTKLIPDSCRRIK 120
DB 61 VCSVALFFYFRAQMDPNRISDEGTHCIYRIILHLENADFDTTLESQDTKLIPDSCRRIK 120
OY 121 CAFQGAQVQKELOHYGSOHIREAKAMVDSWIDLAKRSKLEAPRAHITINATDIPSGSH 180
DB 121 CAFQGAQVQKELOHYGSOHIREAKAMVDSWIDLAKRSKLEAPRAHITINATDIPSGSH 180
OY 181 KYSLSSWYHDMGAKISNMTFSGKLIYNODGFYLYLANICRHHETSGDLATEFLQLMV 240
DB 181 KYSLSSWYHDMGAKISNMTFSGKLIYNODGFYLYLANICRHHETSGDLATEFLQLMV 240
OY 241 VYTKTSIKIPSSHTLMKGSGTKYWSGNSFEHFYSINVGFFKLRSGEETISIEVSNPSLID 300
DB 241 VYTKTSIKIPSSHTLMKGSGTKYWSGNSFEHFYSINVGFFKLRSGEETISIEVSNPSLID 300

DB 241 VYTKTSIKIPSSHTLMKGSGTKYWSGNSFEHFYSINVGFFKLRSGEETISIEVSNPSLID 300
OY 301 PDDQATYFGAFKVDID 317
DB 301 PDDQATYFGAFKVDID 317

RESULT 2
ID TN1L_MOUSE STANDARD; PRT: 316 AA.
AC 035235; 035306;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (osteoclast
DE differentiation factor) (ODF) (osteoclastogenesis-inhibitory factor)
DE (OCIF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hybridoma;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.,
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells."
RL J. Biol. Chem. 272:25190-25194(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=9818248; PubMed=9520411;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.D.,
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation."
RL Cell 93:165-176(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow stroma;
RX MEDLINE=9818248; PubMed=9520411;
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A.,
RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.,
RT "Osteoclast differentiation factor is a ligand for
RT osteoprotegerin/Osteoclastogenesis-inhibitory factor and is identical
RT to TRANCE/RANKL."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymic lymphoma;
RX MEDLINE=96032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.,
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function."
RL Nature 390:175-179(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Ikeda T.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL

```


CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC TRABECULAR BONE AND LUNG.
CC -1- DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBOLO-
CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC OF NEONORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOECTOSIS, WITH
CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC HYPERTROPHIC CHONDROCYTES.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL: AF053713; AAC40113.1; -
CC EMBL: AF013170; AAC71061.1; -
CC EMBL: AB008426; BAA25425.1; -
CC EMBL: AF019048; AAB6812.1; -
CC EMBL: AB036798; BAA37259.1; -
CC MGD: MGI:1100089; Tntsf11
CC Interpro: IPR003263; TNF_5
CC Interpro: IPR000478; TNF_family.
CC Pfam: PF00229; TNF_1.
CC ProDom: PD008600; TNF_5; 1.
CC SMART: SM00207; TNF_1.
CC PROSITE: PS00251; TNF_1; FALSE_NEG.
CC PROSITE: PS0049; TNF_2; 1.
CC Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
CC Signal-anchor.
CC KW SIGNAL-ANCHOR.
CC FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
CC FT DOMAIN 1 48 (POTENTIAL).
CC FT DOMAIN 1 48 (POTENTIAL).
CC FT CARBOHYD 197 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 99 99 G->D (IN REF. 4).
CC FT CONFLICT 99 99 G->D (IN REF. 4).
CC SQ SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

Query Match 84.1%; Score 1417.5; DB 1; Length 316;
Best Local Similarity 84.3%; Pred. No. 3.9e-113;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

OY 1 MRRASRDYTKTLRGSEEGGCGAPHEGRLH-APPAPAPHPAPASRSMFALLGLGIGQ 59
DB 1 MRRASRDYTKTLRGSEEGGCGAPHEGRLH-APPAPAPHPAPASRSMFALLGLGIGQ 60
OY 60 VVCSALFFPYRAQMDPRISSEDGTHCYRLRLHENAADFQDTTLESQDTKLIPDSCARI 119
DB 61 VVCSALFFPYRAQMDPRISSEDGTHCYRLRLHENAADFQDTTLESQDTKLIPDSCARI 118
OY 120 KOAFQAGVQKELQHIYVSGHTRAEKAWDGSMDLAKRSKLEAPPAHLTTNATDIRSGS 179
DB 119 KOAFQAGVQKELQHIYVSGHTRAEKAWDGSMDLAKRSKLEAPPAHLTTNATDIRSGS 178
OY 180 HKVSLSSVYHNRGNVAKISNMTFSNGKLIVNDGFEYUUYANICFRHHETSGDLATEYQOLM 239
DB 179 HKVSLSSVYHNRGNVAKISNMTFSNGKLIVNDGFEYUUYANICFRHHETSGDLATEYQOLM 238
OY 240 VVYVTKTSIKIISSTHTLMKGGSTKWSGSEPHFYISVNGGFFKLRSGEISIVSNPSLL 299
DB 240 VVYVTKTSIKIISSTHTLMKGGSTKWSGSEPHFYISVNGGFFKLRSGEISIVSNPSLL 299

DB 239 VVYVTKTSIKIIPSSHNLMKGGSTKWSGSEPHFYISVNGGFFKLRSAGEISIVSNPSLL 298
OY 300 DPDDQATYFGAFKVDID 317
DB 299 DPDDQATYFGAFKVDID 316

RESULT 3
TN10_HUMAN STANDARD: PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN TNFSF10 OR TRAIL OR Apo2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-10542098; PubMed-8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis".
RL Immunity 3:673-682(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96278649; PubMed-8663110;
RA Pitti R.M., Masters S.A., Ruppert S., Donahue C.J., Moore A.,
RA Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family.";
RL J. Biol. Chem. 271:12687-12690(1996).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX MEDLINE-20017054; PubMed-10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5".
RL Mol. Cell 4:563-571(1999).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed-10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Sreathon G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation".
RL Nat. Struct. Biol. 6:1048-1053(1999).
CC -1- FUNCTION: INDUCES APOPTOSIS.
CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
CC AND PROSTATE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL: U37518; AAC50332.1; -
CC EMBL: U57059; AAB01233.1; -
CC MIM: 603598; -

DR PDB; 1D0G; 22-OCT-99.
 DR PDB; 1D4V; 01-NOV-99.
 DR InterPro; IPR003263; TNF_5.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR00478; TNF_family.
 DR Pfam; PF00229; TNF_1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR ProDom; PD008600; TNF_5; 1.
 DR SMART; SM00207; TNF_1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CycloLine; Transmembrane; Signal-anchor; Apoptosis; 3D-structure.
 KM DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
 SO SEQUENCE 281 AA; 32509 MW; DDAAAF78DAB2F6D CRC64;

Query Match 14.9%; Score 251.5; DB 1; Length 281;
 Best Local Similarity 24.1%; Pred. No. 3.7e-14; Mismatches 117; Indels 45; Gaps 10;
 Matches 71; Conservative 61;

DB 42 PAASSMEVALLGLGVCSVALFFYFRQMD--PRLSEDTGHCITRLRLHENDAF 99
 10 PSLGOTCVLIIVFTVLLSLCAVAVTYFTNLKQMDKYSKSGIACF-----LKED--- 61
 100 QDTLESODTKLIPDSRRIRKQAFQCAVQKELQHTIVGSOHTRAEKAMVDGSLDAKSK 159
 62 -DSYMDPNDEESMNSPCWQVKW-----QLKQLVTKMLTLTSETI-----STVQEKQ 107
 160 LEAQP-----AHLT-----INATDIPSGSHKVSLS--SSWYHDR-GMAKISNM 199
 108 QNISPVLVREGRQVRAAHITGRGNSNTLSSNSKNEKALGKINSWESRGHGFSLNL 167
 200 TFSNGKLIYNQDGFYLLYANICFRHETSGDLATEYLQIMVYVTKSTIKIPSSHTLMKG 259
 168 HLRNGELVHEKGFYIYQTFREFQEEIKENTKNDKQWQVYIKYT--SYDPDILMNSA 226
 260 STRKYSNGSEFHFYSINVGFEKLSGEISIEVSNPLDDPDODATYGAKV 313
 227 RNSCWSKAEYGLYSIYGGIFELKENDRIEVSVTNEHLDMDEASFGAPLV 280

RESULT 4
 TN10_MOUSE STANDARD; PRT; 291 AA.
 ID TN10_MOUSE
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C.A., Goodwin R.G.;
 RT Identification and characterization of a new member of the TNF family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 CC -1- FUNCTION: INDUCES APOPTOSIS.
 CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC -----
 DR EMBL; U37522; AAC52345.1; -
 DR MGI; 107414; Tnfsf10.
 DR InterPro; IPR003263; TNF_5.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR00478; TNF_family.
 DR Pfam; PF00229; TNF_1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR ProDom; PD008600; TNF_5; 1.
 DR SMART; SM00207; TNF_1; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CycloLine; Transmembrane; Signal-anchor; Apoptosis.
 KM DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.7%; Score 248; DB 1; Length 291;
 Best Local Similarity 25.4%; Pred. No. 7.7e-14; Mismatches 100; Indels 80; Gaps 13;
 Matches 79; Conservative 52;

DB 46 RSMFEVALLGLGQVCSVALFFYFRQMD--PRLSEDTGHCITRLRLHENDAFDT 102
 17 RMNVICIVLLQVLLQAVAVTYMTFMKQLODYSKIGLACFSK-----TDEDWDS 71
 103 TLESODTKLIPDSRRIRKQAFQCAVQKELQHTIVGSOHTRAEKAMVDGSLDAKSK 131
 72 T-----DGLINPCLQVNRKQLYLEVTLTFTQDTISTVEKQLSTPLPRGRAPQVA 127
 132 QHIVGSOHTRAEKAMVDGSLDAKSKLEAPFAHLTINATDIPSGSHKVSLSWYHDR 191
 128 AHITGTR-RSNSALI-----PISKDGKTLGQ-----KIESMESSR 162
 192 -GWAKISNMKTSNGKLIYNQDGFYLLYANICFRHETSGDLATEYL-----QLMYV 242
 163 KGHSEFLNHLFRNGELVLEQEGLYIYQTFREFQEAD--ASKWVSQDKVTKQLQVYI 220
 243 TKTSTIKIPSSHTLMKGGSTKYSNGSEFHFYSINVGFEKLSGEISIEVSNPLDDPD 302
 221 YVYT--SYDPPIYLMKSARNSCRDAEYGLYSIYGGIFELKKNDRIVSVTNEHLMDD 279
 303 QDATYFGAKV 313
 280 QEASFGAPLI 290

RESULT 5
 FASL_HUMAN STANDARD; PRT; 281 AA.
 ID FASL_HUMAN
 AC P48023;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FAS antigen ligand (Apoptosis antigen ligand) (APL) (CD178 antigen).
 GN TNFSF6 OR APTL1G1 OR FASL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95105731; PubMed=7528780;
 RA Alderson M.;
 RT "Fas ligand mediates activation-induced cell death in human T

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RT   lymphocytes".;
RL   J. Exp. Med. 181:71-77(1995).
RN
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95127560; PubMed=7826947;
RA   Takehashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT   "Human Fas ligand: gene structure, chromosomal location and species
    specificity.";
RL   Int. Immunol. 6:1567-1574(1994).
RN
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Schaeuble C.E., Pöhlmann R., Philippson P., Etbel H.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95071350; PubMed=7980502;
RA   Mita E., Hayashi N., Iio S., Takehara T., Hijikata T., Kasahara A.,
RT   "Role of Fas ligand in apoptosis induced by hepatitis C virus
    infection.";
RL   Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Wilkinson J.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN
RN   [6]
RP   SEQUENCE OF 1-10 FROM N.A.
RA   Tissue-Blood;
RA   Matsunura M., Nakatsishi Y., Ohba Y.;
RT   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -I- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
    TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
    CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
    FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
    PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
    T CELLS, OR BOTH.
CC   -I- SUBUNIT: HOMODIMER (PROBABLE).
CC   -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
    INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
    SURFACE.
CC   -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   -I- DATABASE: NAME=PROW; NOTE=CD guide CD178 entry;
    WWW="http://www.ncbi.nlm.nih.gov/prow/guide/3338769674.g.htm".
CC
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    or send an email to license@isb-sib.ch).
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DR   EMBL; X89102; CAAG1474.1; -.
DR   EMBL; U08137; AAC50071.1; -.
DR   EMBL; U11821; AAC50124.1; -.
DR   EMBL; D38122; BAA07320.1; -.
DR   EMBL; Z96050; CAB09424.1; -.
DR   EMBL; AB013303; BAA32542.1; -.
DR   HSSP; P06804; 2TNF.
DR   MIW; L34638; -.
DR   InterPro; IPRO03263; TNF_5.
DR   InterPro; IPRO03636; TNF_abc.
DR   InterPro; IPRO00478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_abc; 1.
DR   ProDom; PD008600; TNF_5; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;
    Antigen.
KW   DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).
KT   TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

```

| FT | DOMAIN | 103 | 281 | EXTRACELLULAR (POTENTIAL). |
|-----|---|---------|-----------|-------------------------------------|
| FT | DOMAIN <td>4</td> <td>70</td> <td>PRO-RICH.</td> | 4 | 70 | PRO-RICH. |
| FT | DOMAIN <td>45</td> <td>65 *</td> <td>POLY-PRO.</td> | 45 | 65 * | POLY-PRO. |
| FT | DISULFID <td>202</td> <td>233</td> <td>BY SIMILARITY.</td> | 202 | 233 | BY SIMILARITY. |
| FT | CARBOHYD <td>184</td> <td>184</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td> | 184 | 184 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD <td>250</td> <td>250</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td> | 250 | 250 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD <td>260</td> <td>260</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td> | 260 | 260 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| SEQ | SEQUENCE | 281 AA; | 31485 MW; | ABA6EB358246E9DB CRC64; |

| Query Match | 11.28; | Score 189; | DB 1; | Length 281; |
|-----------------------|------------------|--------------------|-------------|-------------|
| Best Local Similarity | 21.7%; | Pred. No. 7.6e-09; | | |
| Matches 69; | Conservative 43; | Mismatches 98; | Indels 108; | Caps 11; |

| ID | FASTL_MOUSE | STANDARD: | PRT: | 279 AA. |
|----|--|-----------|------|---------|
| AC | PA1047: 061217; Q9R1F2; | | | |
| DT | 01-FEB-1995 (Rel. 31, Created) | | | |
| DT | 01-FEB-1995 (Rel. 31, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | FAS antigen ligand. | | | |
| GN | TNFSF6 OR APRIL1G OR FASL OR GLD. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_Taxid:10090; | | | |
| RN | [1] | | | |
| RN | SEQUENCE FROM N.A. (ISOFORM FASL). | | | |
| RX | MEDLINE=94185175; PubMed=7511063; | | | |
| RA | Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G., | | | |
| RA | Suda T., Nagata S.; | | | |
| RT | "Generalized lymphoproliferative disease in mice, caused by a point | | | |
| RT | mutation in the Fas ligand."; | | | |
| RL | Cell 76:969-976(1994). | | | |
| RN | [2] | | | |
| RN | SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING. | | | |
| RC | SPRAIN-C57BL/6; | | | |
| RX | MEDLINE=95386076; PubMed=7544870; | | | |
| RA | Peitsch M.J., Tschopp J.; | | | |
| RT | "Comparative molecular modelling of the Fas-ligand and other members | | | |
| RT | of the TNF family."; | | | |
| RL | Mol. Immunol. 32:761-772(1995). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM FASL). | | | |
| RX | MEDLINE=95196085; PubMed=789405; | | | |
| RA | Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E., | | | |
| RA | Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.; | | | |

RT "the mouse Fas-ligand gene is mutated in gld mice and is part of a
TNF family gene cluster."
Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RC STRAIN-BALB/C;
RA Fennner M.H., Shioda T., Isselbacher K.J.;
RT "two musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids."
RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM FASLS).
RC STRAIN-C3H; TISSUE-Spleen;
RX MEDLINE=20021694; Pubmed=10552956;
RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: A new alternatively
RT spliced product of the mouse Fas ligand gene."
RL Blood 94:3456-3467(1999).
RN [6]
RP CHARACTERIZATION OF VARIANT GLD.
RX MEDLINE=9609192; Pubmed=7495745;
RA Hahne M., Peltsch M.C., Imtler M., Schroeter M., Lowin B.,
RA Rousseau M., Bron C., Renno T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice."
RL Int. Immunol. 7:1381-1386(1995).
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN. A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.
CC ISOFORM FASLS IS SOLUBLE.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
CC WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
CC INTERACTION.
CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL: U06948; AAA17800.1; -
DR EMBL: U10984; AAA19778.1; -
DR EMBL: S76752; AAB33780.1; -
DR EMBL: U58995; AAB02915.1; -
DR HSSP: AF119335; AAD52106.1; -
DR HSSP: P01375; 4TSV
DR MGD; MGI:99255; Tnfsf6
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1;
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;
KW Disease mutation; Alternative splicing
FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 4 69 PRO-RICH.
FT DOMAIN 45 51 POLY-PRO.
FT DISULFID 200 231 BY SIMILARITY.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 210 MISSING (IN ISOFORM FASLS).
FT VARIANT 184 184 T -> G (IN STRAIN BALB/C).
FT VARIANT 218 218 E -> A (IN STRAIN BALB/C).
FT VARIANT 273 273 F -> L (IN GLD); ABOLISHES BINDING OF FASL
FT VARIANT 273 273 TO ITS RECEPTOR.
SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;
Query Match 10.98; Score 184.5; DB 1; Length 279;
Best Local Similarity 21.7%; Pred. No. 1.8e-08;
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;
QY 13 RGSEMGGPGAPHEGPHLAPPPAPHP-----PAASRMFVALLGL 57
DB 38 RGPQRRPPPPPPVSPLPSPPLPLPLKKNHNTMLPVYFENVYALVGMGL 97
QY 58 GQVVCVAAEFYFRAQMDPNRISEDTGHCYRILRLHENDFQDTLESQDTKLIPSCR 117
DB 98 G-----MYLFHL----- 105
QY 118 RIKAFQAGVOKELQHT--VGSQHIRA---EKAVDSSMDLAKRSKLEQFAHLITNA 172
DB 106 -----OKELAELEFNTOSLKVSFEKQIANS---TPSEKREPSVAHLIGN- 150
QY 173 TDIPSGSHKVSLS-SWYHDRGMKISMNTEFNGKLIYNDGFYLYANICFRHETSGDL 231
DB 151 -----PHSRSLPLEMEDYGTALISGVKKGLVINEGLYVYKYVFRGSGCN--- 201
QY 232 ATEYLQMLVYTKTSIKIPSSHTLMKGSGTKYWSGNSFPHYSINVGCFKLNGSEISI 291
DB 202 -NQLNKHVYWRNS--KYPEDLVIMEERKLNYCT-TQOIMHSSYTLGAVNLTSADHLVY 257
QY 292 EVSNPSILDPDQDATYFGAFKV 313
DB 258 NISQSLINEESKTEFGLYKL 279
RESULT 7
ID TNF5_BOVIN STANDARD; PRT; 261 AA.
AC PS1749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen
DE GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96006582; Pubmed=7590981;
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RT and tumor necrosis factor alpha."
RL Immunogenetics 42:430-431(1995).
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).

```

CC -1 SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL; 248469; CAA8363.1; .
DR HSSP; P29965; IALY.
DR InterPro; IPR003263; TNF_5
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
KW DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT DOMAIN 47 261 EXTRACELLULAR (POTENTIAL).
FT DISULFID 178 218 POTENTIAL.
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 261 AA: 29242 MW: 8491FEFB30A787FD CRC64:

Query Match 10.5%; Score 176.5; DB 1; Length 261;
Best Local Similarity 24.2%; Pred. No. 7.9e-08;
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

OY 33 PPPAPHPAPASRSMFVALGLG-GOVCSVALFFFRQMDPRISDGTICIRIL 91
DB 8 PPSRVATGPRVSMKIFMYLLVFLITQMIGSALFAVYLHRLD-KIIDE-----R 57
OY 92 RHENANDODT--LESODTKLIPDSCKRIKQAFQAVOKELQHTVSGOHTRAEKAVDG 149
DB 58 NHDEFVFMKTLQRCNKEGSLSLNCEIRSFEDLVKDIQO---KKEVKKKKKEKE- 112
OY 150 SWLDLAKRSKLEAPFAHLITMATDIPSGSHKVSLSWYHGRMAKIN--MTFENGR-L 206
DB 113 -----MHKGDEPQIAIAIVISAS-----SKTTSVLQW-APRGYTTLSNNLVLENGKQL 161
OY 207 IVNODGFYLYVANICFRHHTSGDLATEYLDLMVYVTKTSIKIP--SSHTLKKGGSTKYW 264
DB 162 AVKRGGFYIYTOVTFCSNR-----ETLSQAPFIASLCKSPSGSRILLRAANTH-- 212
OY 265 SGNSEFHYSINVGFFKLRSGEISIVSNPSLDPDQATYFGAFKV 313
DB 213 SSSKPCGGQSIHLGQFVLQSGASVFNVTDPQVSHGTGFTSFLKL 261

RESULT 8
FASTL_RAT STANDARD; PRT; 278 AA.
AC P36940.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FAS antigen ligand
GN TNFSF6 OR AP11LGI OR FASL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94084792; Pubmed=7505205;
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the fas ligand, a novel member
of the tumor necrosis factor family.";

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RL Cell 75:1169-1178(1993).
CC -1 FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN. A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -1 SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID. PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -1 INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -1 SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL; U03470; AAC52129.1; .
DR HSSP; P01375; AFSV.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
KW DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 69 PRO-RICH.
FT DOMAIN 45 58 POLY-PRO.
FT DISULFID 199 230 BY SIMILARITY.
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 278 AA: 31140 MW: 2898E18A862CEAC6 CRC64:

Query Match 10.4%; Score 175.5; DB 1; Length 278;
Best Local Similarity 20.3%; Pred. No. 1e-07;
Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

OY 21 GPGAPHEGLHAPPAPHPAPASRSM-----FVALGLGL 57
DB 39 GPGGRPPPP--PPPPSPPLPPSPQPLPLPLKKNIEMLPVFFMVLVALVGMGL 96
OY 58 GOVCSVALFFERYAKQMDPRISDGTICIRILRHENADPDOTLESODTKLIPSCR 117
DB 97 G-----WQFLQKELAELEFETNHSL-RVSSFEKQIANDSTBETKRPSSV----- 143
OY 118 RIKQAFQAVOKELQHTVSGOHTRAEKAVDGSWLDLAKRSKLEAPFAHLITMATDIPS 177
DB 144 -----AHLTONPR----- 151
OY 178 GSHKVSLSWYHGRMAKISMTFSNCKLLVNDGFYLYVANICFRHHTSGDLATEYLD 237
DB 152 -SRSLP-EMEDYTGALISGVKKGGIYINAGLYFVYSKYVFGQSCN---SQPLS 205
OY 238 LMVYVTKTSIKIPSSHLMKMGSTKYSGNSEFHFYSINVGFFKLRSGEISIVSNPS 297
DB 206 HKYVM--RNKKYGGDLVMEKKLNCT-TGQIAHSSYLGAVFNLTVDHLVYNISQLS 262

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OY 298 LIDPODATTYFARKV 313
 Db 263 LINEESTKFEGLYKL 278

RESULT 9
 TNFS_HUMAN STANDARD: PRT: 261 AA.
 ID TNFS_HUMAN
 AC P29965;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CD40 ligand (CD40-L) (TNF-related activation protein) (TRAP) (T cell antigen GP39) (CD154 antigen)
 DE TNFS5 OR CD40LG OR CD40L OR TRAP.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCHI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93076854; PubMed=1280226;
 RA Graf D., Korthauer U., Mages H.W., Seenger G., Kroczeck R.A.;
 RT "Cloning of TRAP, a ligand for CD40 on human T cells.";
 RL Eur. J. Immunol. 22:3191-3194(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93049181; PubMed=7678782;
 RA Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,
 RA Briesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,
 RA Aruffo A.;
 RT "The human T cell antigen gp39, a member of the TNF gene family, is a ligand for the CD40 receptor: expression of a soluble form of gp39 with B cell co-stimulatory activity.";
 RL EMBO J. 11:4313-4321(1992).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.
 RX MEDLINE=93145330; PubMed=7678782;
 RA Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A.,
 RA Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,
 RA Macculif B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
 RT "Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion.";
 RL J. Exp. Med. 176:1543-1550(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93094757; PubMed=1281209;
 RA Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,
 RA Macculif B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
 RT "Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion.";
 RL J. Exp. Med. 176:1543-1550(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93138085; PubMed=7678552;
 RA Gauchat J.F.M., Aubry J., Mazzei G.J., Ilfe P., Jomotte T., Elson G.,
 RA Bonnefoy J.Y.;
 RT "Human CD40 ligand: molecular cloning, cellular distribution and regulation of expression by factors controlling IgE production.";
 RL Leuk. 315:259-266(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,
 RA Matsuda I.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
 RX MEDLINE=96131874; PubMed=858998;
 RA Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
 RA Chess L., Thomas D.;
 RT "2-A crystal structure of an extracellular fragment of human CD40 ligand.";
 RL structure 3:1031-1039(1995).

RN [8]
 RP 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.
 RX MEDLINE=98266353; PubMed=9605317;
 RA Singh J., Garber E., Van Vlijmen H., Karpusas M., Hsu Y.-M.,
 RA Zheng Z., Naismith J.H., Thomas D.;
 RT "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";
 RL Protein Sci. 7:1124-1135(1998).
 RN [9]
 RP VARIANTS HIGM1 ARG-36 AND GLY-140.
 RX MEDLINE=93136839; PubMed=7679206;
 RA Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,
 RA Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,
 RA Kroczeck R.A.;
 RT "Defective expression of T-cell CD40 ligand causes X-linked immunodeficiency with hyper-IgM.";
 RL Nature 361:539-541(1993).
 RN [10]
 RP VARIANT HIGM1 GLU-123.
 RX MEDLINE=93156840; PubMed=8094231;
 RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,
 RA de Saint Basile G.;
 RT "CD40 ligand mutations in x-linked immunodeficiency with hyper-IgM.";
 RL Nature 361:541-543(1993).
 RN [11]
 RP VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227.
 RX MEDLINE=93174270; PubMed=7679801;
 RA Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,
 RA Copeland N.G., Bedell M.A., Edelhoff S., Distche C.M.,
 RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;
 RT "CD40 ligand gene defects responsible for X-linked hyper-IgM syndrome.";
 RL Science 259:990-993(1993).
 RN [12]
 RP VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
 RX MEDLINE=95233438; PubMed=7717401;
 RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnoli D.,
 RA Gillani S., Mantuano E., Fasth A., Andersson B., Zegers B.D.M.,
 RA Cavagni G., Reznick I., Levy J., Zan-Bar I., Porat Y., Airo P.,
 RA Plebani A., Vezzoni P., Notarangelo L.D.;
 RT "Characterization of nine novel mutations in the CD40 ligand gene in patients with X-linked hyper IgM syndrome of various ancestry.";
 RL Am. J. Hum. genet. 56:898-906(1995).
 RN [13]
 RP VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219.
 RX MEDLINE=96133533; PubMed=8550833;
 RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,
 RA Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.;
 RT "A single strand conformation polymorphism study of CD40 ligand. Efficient mutation analysis and carrier detection for X-linked hyper IgM syndrome.";
 RL J. Clin. Invest. 97:196-201(1996).
 RN [14]
 RP VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.
 RX MEDLINE=97295077; PubMed=9150729;
 RA Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neuhauer M.,
 RA Yata J.-I., Och H.D.;
 RT "Mutations of the CD40 ligand gene in 13 Japanese patients with X-linked hyper-IgM syndrome.";
 RL Hum. Genet. 99:624-627(1997).
 RN [15]
 RP FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
 CC -1 SUBUNIT: HOMOTRIMER.
 CC -1 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
 CC -1 TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+ T-LYMPHOCYTES.
 CC -1 DISEASE: DEFECTS IN TNFS5 ARE THE CAUSE OF AN X-LINKED IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1). AN IMMUNOGLOBULIN ISOTYPE SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)

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CC RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
CC PNEUMOCYSTIS CARINITI PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
CC CRAPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
CC INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
CC WITH A DEATH RATE OF ABOUT 10% AFTER ADOLSCENCE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -1- DATABASE: NAME-CD40L defect database (mutation db);
CC NOTE-European CD40L defect database (cd40lbase/);
CC WWW="http://www.expasy.org/cd40lbase/";
CC -1- DATABASE: NAME-PRO: NOTE-CD guide CD154 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd154.htm".
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CC -----
DR EMBL: X68550; CAA48554.1; -
DR EMBL: 215017; CAA78737.1; -
DR EMBL: X67878; CAA48077.1; -
DR EMBL: L07414; AAA35662.1; -
DR EMBL: D31797; BAA06599.1; -
DR EMBL: D31793; BAA06599.1; JOINED.
DR EMBL: D31794; BAA06599.1; JOINED.
DR EMBL: D31795; BAA06599.1; JOINED.
DR EMBL: D31796; BAA06599.1; JOINED.
DR PIR: S25684; S25684.
DR PIR: S26694; S26694.
DR PIR: S28017; S28017.
DR PIR: S28852; S28852.
DR PIR: JH0793; JH0793.
DR PDB: 1ALY; 17-SEP-97.
DR MIM: 308230; -
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50045; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; 3D-structure;
KW Antigen; Disease mutation; Polymorphism.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 47 261 EXTRACELLULAR (POTENTIAL).
FT DISULFID 178 218 POTENTIAL.
FT CARBOHYD 240 240 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 36 36 M->R (IN H1GM1).
FT VARIANT 123 123 /FTID-VAR_007513.
FT VARIANT 126 126 A->E (IN H1GM1).
FT VARIANT 126 126 /FTID-VAR_007514.
FT VARIANT 126 126 V->A (IN H1GM1).
FT VARIANT 128 129 /FTID-VAR_007515.
FT VARIANT 128 129 SE->RG (IN H1GM1).
FT VARIANT 140 140 /FTID-VAR_007516.
FT VARIANT 140 140 W->C (IN H1GM1).
Query Match 9.4%; Score 158.5; DB 1; Length 261;
Best Local Similarity 24.5%; Pred. No. 2.7e-06;
Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;
```

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QY 45 SRSFVALTGLT-GGVVCSVALFFYPRAQMDPNRISDGHCIYRLRLRHENADPDQT- 102
DB 20 SMKIFMFLVFLITOMIGSLNPAVYLHRRKD-KTIDE-----RNLDHEDVEFKTI 69
QY 103 -TLESODTKLPDSCRRIKAFQAVOKLOHIYGOHRAEKAMVDGWSWDLAKRSKLE 161
DB 70 QRCWTGSRSLNLCNEIKSOFEGFV-KDLM-----LKEETKKKNSF-EMQKGDQ-N 119
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QY 162 AQPFAHLTINATDIPSGSHKVSLSWYHDSMAKISN--MTFSNGK-LIYNODGFYLYA 218
DB 120 PQLAAHAYSESS-----SKTTSVLQW-AEKGYMNNVLLENGKQLPYKQGLYYIA 173
QY 219 NICEFHHTSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGSTKYWNSGFHFYSIN 276
DB 174 QVTFCSNRBAASQAP-----FTASLCIKSPGFEHILRAANTH--SSAKPGQGSIH 224
QY 277 VGGFFKLRSGEIEIENSNPLDPPDDATYFGAFKV 313
DB 225 LGVFEILQPGASVFNVTDPDSQVSHGTGFTSGFLKL 261
```

RESULT 10

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TNFS_FELCA
ID TNFS_FELCA STANDARD; PRT; 260 AA.
AC 097605;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD40 ligand (CD154 antigen).
GN TNFSF9 OR CD40LG OR CD40L.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Hosie M.J., Willett B.J.;
RT "Adjuvant properties of feline CD154 (CD40 ligand).";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF079105; AAD02954.1; -
DR HSSP: P29965; 1ALY.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 47 260 EXTRACELLULAR (POTENTIAL).
FT DISULFID 177 217 POTENTIAL.
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 260 AA; 28727 MW; 3439A0391B7B932 CRC64;
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QY 32 APPPAHPDPAASRSMFVALTGLT-GGVVCSVALFFYPRAQMDPNRISDGHCIYRI 90
Query Match 9.0%; Score 152; DB 1; Length 260;
Best Local Similarity 23.4%; Pred. No. 9.5e-06;
Matches 68; Conservative 55; Mismatches 121; Indels 46; Gaps 14;
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```

Db 9 APR5AP--GPPVSKITMYLITVLTOMIGSALFANYLRRD--KIEE-----56
QY 91 LRLEHNAFODTLESQ--DTKLIPDSCRRKIOAFQAVORELOHIVSGHIREKAVND 148
Db 57 RNLYEDFVFMKTLQCNKGEGALSLNCEEIKSPFEAF---LKIMLNKTKKKNVA- 111
QY 149 GSWLDLARKSLKLEOPFHLITNADIDISSGSHKVSLSWYHDRCNAKISN--MFESNGK- 205
Db 112 -----MKGGDOPRVAAHVISEAS-----SSTASVLQW-APKGYTTSNLTVLNKGQ 159
QY 206 LIVNODGFYVLYANICFRHNETSGDLATEYLQWVYTKTSIKIP--SSHTLMKGGSTKY 263
Db 160 LAVKROGLIYIAQVTFCSNRASQAP-----FISLCHSPSGSERVLLRANMR- 211
QY 264 WSGNSEFHFYSINVGFFKLRSGEISIEVSNPSLLDPDQATYTGAFKV 313
Db 212 -SSKPCGQGSITLGGVELHFGASVFNWVDPDSQVSHGTGFTSPGLKL 260

RESULT 11
TNFA_CAVPO STANDARD: PRT: 234 AA.
AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
GN TNF OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognath; Cavidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DUNKIN-HARTLEY;
RX MEDLINE=97462215; PubMed=9316485;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
factor-alpha.";
RL Am. J. Physiol. 273:1524-1530(1997).
CC -I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -I- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -I- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U39839; AAB06492.1; -
CC DR EMBL: U77036; AAB19210.1; -

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DR HSP; P06804; 2TNF.
DR InterPro: IPR003636; TNF-abc.
DR InterPro: IPR000478; TNF-family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF-abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine; Cytotoxicity; Transmembrane; Glycoprotein; Signal-anchor.
KW CYCLOKIN; PROPEP 1
FT CHAIN 80 234 BY SIMILARITY.
FT TRANSMEM 36 56 TUMOR NECROSIS FACTOR.
FT DISULFID 147 178 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 8.7%; Score 146; DB 1; Length 234;
Best Local Similarity 25.4%; Pred. No. 2,7e-05;
Matches 50; Conservative 30; Mismatches 75; Indels 42; Gaps 8;

QY 134 IVSGHITAEKAMVDGSLDLAKRSKLEA-----QPFHLITNADIDIPSGSHKVSLS 186
Db 55 VIGPQ--REDFSSGPPRPILAQTLLRSASQNDKRVAAHVAN-----QQAEEELQ 105
QY 187 WYHDGMAKISN-MTFNGKLIIVNODGFYVLYANICFRHNETSGDLATEYLQWVYTKT 245
Db 106 WLSKRAMNLLNMGMLSDNQLVPSDGLYLSQVLFK-----GQGCPSYLLTHTVSRL 160
QY 246 SIKIPSSHFLM-----KGGSTKYWSGNSFHFYSINVGFFKLRSGEISIEV 293
Db 161 AVSYPERKVNLLSAIKSPCKETPECAERKPV-----YEDYLGAVQLQGRLSAEV 213
QY 294 SNPSLLD-PDQATYFG 309
Db 214 NLPQYLDPRADSGQIYFG 230

RESULT 12
TNFS_CANFA STANDARD: PRT: 260 AA.
AC O97626;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD40 ligand.
GN TNFSF5 OR CD40LG OR CD40L.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Hosie M.H., Willeit B.J.;
RT Adjuvant properties of canine CD40L.";
RL Submitted (A05-1998) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -I- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF086711; AAD04375.1; -
CC DR

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CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL: U06950; AAA18594.1; -
DR EMBL: M13049; AAA40457.1; -
DR EMBL: M11731; AAA40458.1; -
DR EMBL: Y00467; CAA68530.1; -
DR EMBL: X02611; CAA26457.1; -
DR EMBL: M20155; AAA40462.1; ALT_SEQ.
DR EMBL: M38296; AAA40459.1; -
DR EMBL: D84196; BAA19512.1; -
DR EMBL: D84194; BAA19512.1; JOINED.
DR EMBL: D84195; BAA19512.1; JOINED.
DR EMBL: D84199; BAA19513.1; -
DR EMBL: D84197; BAA19513.1; JOINED.
DR EMBL: D84198; BAA19513.1; JOINED.
DR PIR: A23127; QMNSN.
DR PIR: A22908; A22908.
DR PIR: A25164; A25164.
DR PIR: A27303; A27303.
DR PIR: A34251; A34251.
DR PIR: S03791; S03791.
DR PDB: 2TNF; 12-OCT-99.
DR MGD: MGI:104798; TNF.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR Cytokine: Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
KW 3D-structure.
FT PROPEP 1 79
FT CHAIN 80 235 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 148 179
FT CARBOHD 86 86 N-LINKED (GLCNAC. . .).
FT CONFLICT 231 231 G->R (IN REF. 3 AND 4).
SQ SEQUENCE 235 AA; 25895 MM; 16DD2A9676D68C5D CRC64;

Query Match 8.4%; Score 141.5; DB 1; Length 235;
Best Local Similarity 25.9%; Pred. No. 6.5e-05;
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

Oy 163 QPFAHLLTNADIPSGSRKYSLS-SWYHNRGAKISN-WTFENGKLIYNQDFFYLYANI 220
Db 90 KPAHVAN-----HQVEQLEWLSQRAVALLLANGMDLNDLVVPADSLYLYSOV 141
Oy 221 CRRHETSGLATEYLIQIMVYTK-----TSIKIPSSHILMKSGSTKYWSGNS 268
Db 142 LFK-----GGGCPDYVLLTHYVSRAISYQEKVNLISAVKSCPPDTEGALFKW----- 192

Oy 269 EHFYSINVGFKKRSGEISIEVSNPSLID-PDQATYFG 309
Db 193 --YEPYLVGQVFOLEKGDLSAEVNLPKLYDFAESGQVFG 231

RESULT 14
ID TNFA_RABIT STANDARD; PRT; 235 AA.
AC P04924;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
GN TNF OR TNFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91065534; Pubmed=2249779;
RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA Nosopasov S.A.;
RT "Structural analysis of the rabbit TNF locus, containing the genes
RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT factor).";
RL Gene 95:215-221(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219712; Pubmed=3519138;
RA Ito H., Shirai T., Yamamoto S., Akita M., Kawahara S., Todd C.W.,
RA Wallace R.B.;
RT "Molecular cloning of the gene encoding rabbit tumor necrosis
RT factor.";
RL DNA 5:157-165(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219711; Pubmed=3519137;
RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
RA Hayashi H., Kato M., Seko M.;
RT "Molecular cloning and expression in Escherichia coli of the cDNA
RT coding for rabbit tumor necrosis factor.";
RL DNA 5:149-156(1986).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL: M12845; AAA31486.1; -
DR EMBL: M12846; AAA31482.1; -
DR EMBL: M60340; AAA31484.1; -
DR PIR: A25451; A25451.
DR PIR: A25454; A25454.

| RESULT | 15 |
|-------------|---|
| TFNFA_SHEEP | |
| ID | TFNFA_SHEEP |
| AC | P23383 |
| DT | 01-NOV-1991 (Rel. 20, Created) |
| DT | 01-FEB-1994 (Rel. 28, Last sequence update) |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) |
| DE | Tumor necrosis factor precursor (TNF-alpha) (Cachectin). |
| GN | TNF OR TFNFA. |
| OS | Ovis aries (Sheep). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; |
| OC | Bovidae; Caprinae; Ovis. |
| OX | NCBI_TaxID=9940; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=Liver; |
| RX | MEDLINE=91067496; PubMed=2251151; |
| RA | Young A.J., Hay J.B., Chan J.Y.C.; |
| RT | Primary structure of ovine tumor necrosis factor alpha cDNA.; |
| RL | Nucleic Acids Res. 18:6723-6723(1990). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=Alveolar macrophage; |
| RC | MEDLINE=92112044; PubMed=1765267; |

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0Y  IVS0H1RREKANVDSW---LDLAKRSTLE--QPAHILTATDIPSGSHKVSLSN 187
134  :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db  55  VIGPQ--REQDSFAGTSFNRPLVLOTLRSSQASNNKRPAAHVAVN-----ISAP 100
0Y  188  YHDSGMAKISNMTFSG-----KTIYODGEFYLYANICFRHH-----ETSGUL 231
Db  101  GQLRMDSVANNLMANVCVELKNQVLAVPTDGLVITLYSOVLEFGKGCSPNPLFLHTISRI 160

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Tue Jul 9 13:21:07 2002

us-09-865-363-13.rsp

Page 14

| | | | |
|----|------|---|-------------|
| OY | .232 | A T E Y L Q M V Y V T K T S I K I P S S H L M K G S T I R K Y M S G N S E F F P I A I N O G F P K L L S G E I S T | 291 |
| | | I : : : : : | I : : : : : |
| Dd | 161 | A V S Y - Q T K V N T L I - S K I S P C H R E T L E G A E K P W ----- Y E P I Y G S G V F O L K G D R L S A | 211 |
| | | I : : : : : | I : : : : : |
| OY | 292 | E V S N P S L I D - P D O A T Y F G | 309 |
| | | I : : : : : | I : : : : : |
| Dd | 212 | E T N L P E Y L D Y A E S G O V Y T G | 230 |

Search completed: July 8, 2002, 18:51:50
Job time: 17488 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 8, 2002, 19:52:38 ; Search time 119.9 Seconds
(without alignments)
457,376 Million cell updates/sec

Title: US-09-865-363-13
Perfect score: 1685
Sequence: 1 MRASRDYTYTLRGSEBMG.....LDDPDQATYGAFAKVRDID 317

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL.19:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_fodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------|-------------------------|
| 1 | 1422 | 84.4 | 270 | 4 Q96Q17 | Q96Q17 homo sapien |
| 2 | 1409 | 83.6 | 313 | 11 Q9RIY0 | Q9RIY0 mus musculu |
| 3 | 1396.5 | 82.9 | 318 | 11 Q9SE82 | Q9SE82 ratu mus musculu |
| 4 | 1271 | 75.4 | 287 | 11 Q9JJK8 | Q9JJK8 mus musculu |
| 5 | 909 | 53.9 | 199 | 11 Q9JJK8 | Q9JJK8 mus musculu |
| 6 | 262 | 15.5 | 53 | 11 Q9JJK8 | Q9JJK8 mus musculu |
| 7 | 240.5 | 14.3 | 214 | 13 Q9DDZ5 | Q9DDZ5 brachydanto |
| 8 | 216.5 | 12.8 | 287 | 13 Q9DDZ5 | Q9DDZ5 brachydanto |
| 9 | 200 | 11.9 | 282 | 6 Q9BEA8 | Q9BEA8 sus scrofa |
| 10 | 200 | 11.9 | 282 | 6 Q9BEA8 | Q9BEA8 sus scrofa |
| 11 | 199 | 11.8 | 280 | 6 Q9MYI6 | Q9MYI6 macaca neme |
| 12 | 186 | 11.0 | 280 | 6 Q9BDM5 | Q9BDM5 macaca mula |
| 13 | 184.5 | 10.9 | 280 | 6 Q9BDN1 | Q9BDN1 cerceobus |
| 14 | 182.5 | 10.8 | 281 | 6 Q9BDN3 | Q9BDN3 callithrix |
| 15 | 169.5 | 10.1 | 261 | 6 Q9BDM3 | Q9BDM3 aotus trivi |
| 16 | 167.5 | 9.9 | 261 | 6 Q9BDM3 | Q9BDM3 aotus trivi |

| | | | | | |
|----|-------|-----|-----|-----------|----------------------|
| 17 | 155.5 | 9.2 | 261 | 6 Q9BDC7 | Q9BDC7 macaca mula |
| 18 | 155 | 9.2 | 272 | 13 Q9IBD8 | Q9IBD8 gallus gall |
| 19 | 145.5 | 8.6 | 239 | 11 Q9QYH9 | Q9QYH9 mus musculu |
| 20 | 145 | 8.6 | 174 | 4 Q95150 | Q95150 homo sapien |
| 21 | 144 | 8.5 | 232 | 11 Q35853 | Q35853 mus musculu |
| 22 | 143 | 8.5 | 240 | 6 Q9BDM7 | Q9BDM7 macaca neme |
| 23 | 139.5 | 8.3 | 215 | 11 Q99ND1 | Q99ND1 lamasciuru |
| 24 | 137.5 | 8.2 | 156 | 11 Q91ZL4 | Q91ZL4 sigmodon hl |
| 25 | 136 | 8.1 | 234 | 6 Q28320 | Q28320 capra hircu |
| 26 | 134.5 | 8.0 | 310 | 11 Q9JM10 | Q9JM10 marmota mon |
| 27 | 134 | 8.0 | 157 | 4 Q43647 | Q43647 homo sapien |
| 28 | 134 | 8.0 | 204 | 4 Q96LD2 | Q96LD2 homo sapien |
| 29 | 133 | 7.9 | 149 | 6 Q97543 | Q97543 aotus nancy |
| 30 | 133 | 7.9 | 191 | 6 Q9MYZ2 | Q9MYZ2 capra hircu |
| 31 | 133 | 7.9 | 232 | 4 Q9U1V3 | Q9U1V3 homo sapien |
| 32 | 131.5 | 7.8 | 216 | 11 Q70332 | Q70332 mesocricetu |
| 33 | 130 | 7.7 | 217 | 11 Q9ERK6 | Q9ERK6 peromyscus |
| 34 | 128 | 7.6 | 234 | 6 Q9TTJ3 | Q9TTJ3 equus caball |
| 35 | 127.5 | 7.6 | 217 | 6 Q9BEC5 | Q9BEC5 tenrec ecau |
| 36 | 127.5 | 7.6 | 235 | 11 Q9J127 | Q9J127 ratu mus norv |
| 37 | 127.5 | 7.6 | 235 | 11 Q9J126 | Q9J126 ratu mus norv |
| 38 | 127.5 | 7.6 | 310 | 11 Q9JM11 | Q9JM11 marmota mon |
| 39 | 126 | 7.5 | 149 | 6 Q97538 | Q97538 aotus vocif |
| 40 | 126 | 7.5 | 149 | 6 Q9TTG8 | Q9TTG8 aotus nigri |
| 41 | 125 | 7.4 | 216 | 6 Q9BEC9 | Q9BEC9 ochotona pr |
| 42 | 124 | 7.4 | 250 | 6 Q9XT47 | Q9XT47 macropus eu |
| 43 | 120.5 | 7.2 | 217 | 6 Q9BEC1 | Q9BEC1 bradyopus tr |
| 44 | 120.5 | 7.2 | 217 | 6 Q9BEC0 | Q9BEC0 cyclopes dl |
| 45 | 120 | 7.1 | 260 | 11 Q9Z2V2 | Q9Z2V2 ratu mus norv |

ALIGNMENTS

RESULT 1
ID Q96Q17 PRELIMINARY; PRT; 270 AA.
AC Q96Q17;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HRANKL 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda T., Kuroyama H., Hirokawa K.;
RT "Human RANKL Isoform."
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB061227; BAB71768.1; -; SC7754CE32EF368 CRC64;
SQ SEQUENCE 270 AA; 30522 MW; 5C7754CE32EF368 CRC64;

Query Match 84.4%; Score 1422; DB 4; Length 270;
Best Local Similarity: 100.0%; Pred. No. 1; le-121;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 MFALLGLGLGVCSVALFFFRQMDPNRISEDTGHCIVRIILRHENADPDPTLLESO 107
DB 1 MFALLGLGLGVCSVALFFFRQMDPNRISEDTGHCIVRIILRHENADPDPTLLESO 60
QY 108 DFKLIPDSGRIRKQAFQAVOKELQIVGSOHRAEKAWDGSWIDLAKRSKLEQPPAH 167
DB 61 DFKLIPDSGRIRKQAFQAVOKELQIVGSOHRAEKAWDGSWIDLAKRSKLEQPPAH 120
QY 168 LITNATDIPSGSHKVSLSWYHRCWAKISNMTFSNGKLIYQDGFYLYANICFRHHET 227
DB 121 LITNATDIPSGSHKVSLSWYHRCWAKISNMTFSNGKLIYQDGFYLYANICFRHHET 180
QY 228 SGLPTEYQLWVYTKTSIKIPSSHTLMKGSSTYNSGNSFHHYSINVGFFKLRSGE 287
|||||

RA [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21150053; PubMed-11250921;
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT "Determination of Three Isoforms of the Receptor Activator of Nuclear
RT Factor-kappaB Ligand and Their Differential Expression in Bone and
RT Thymus."
RL Endocrinology 142:1419-1426(2001).
DR EMBL: AB032771; BAA97257.1; -.
DR HSSP: P50591; 1D0G.
DR MGD: MGI:1100089; Tnfef11.
DR InterPro: IPR003263; TNF-5.
DR InterPro: IPR003636; TNF-abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF-abc; 1.
DR ProDom: PD008600; TNF-5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS50049; TNF-2; 1.
SQ SEQUENCE 287 AA; 32234 MW; 8B2CE8EAC7B534CC CRC64;

Query Match 75.4%; Score 1271; DB 11; Length 287;
Best Local Similarity 77.3%; Pred. No. 7.4e-108;
Matches 245; Conservative 16; Mismatches 26; Indels 30; Gaps 2;

QY 1 MRASRDYTYLRLGSEEMGGPGAPHEGPHAPPPAPHPAPASRMFVALLGLGLGOV 60
DB 1 MRASRDYTYLRL-----TPASRMFLALLGLGLGOV 32
QY 61 VCSYALFFYRAQMDPNRISEDTGTCIYRLRLHENADFODTTLSDOTKLIPDSRRIK 120
DB 33 VCSIALFLYFRAQMDPNRISEDTGTCIYRLRLHENAGLDSTLESBDT--LPDSRRMK 90
QY 121 QAFGAVQKELQHYVSGOHLRAEKAMVDGSMIDLAKRSKLEAOPALHTNATDIPSGH 180
DB 91 QAFGAVQKELQHYVSGOHLRAEKAMVDGSMIDLAKRSKLEAOPALHTNATDIPSGH 150
QY 181 KVSLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 240
DB 151 KVTLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 210
QY 241 YVTKTSIKIPSSHTLMKSGSTKYNSEPHFYSINVGFFKLRSGEISIEVSNPSLLD 300
DB 211 YVTKTSIKIPSSHTLMKSGSTKYNSEPHFYSINVGFFKLRSGEISIEVSNPSLLD 270
QY 301 PPDQATYFGAFKVDID 317
DB 271 PPDQATYFGAFKVDID 287

RESULT 5
Q9JUK8 PRELIMINARY; PRT; 199 AA.
ID Q9JUK8;
AC Q9JUK8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-DEC-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 3.
GN TNFSF11 OR RANKL 3
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBL_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21150053; PubMed-11250921;
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT "Determination of Three Isoforms of the Receptor Activator of Nuclear
RT Factor-kappaB Ligand and Their Differential Expression in Bone and
RT Thymus."
RL Endocrinology 142:1419-1426(2001).
DR EMBL: AB032772; BAA97258.1; -.

DR HSSP: P50591; 1D0G.
DR MGD: MGI:1100089; Tnfef11.
DR InterPro: IPR003263; TNF-5.
DR InterPro: IPR003636; TNF-abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF-abc; 1.
DR ProDom: PD008600; TNF-5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS50049; TNF-2; 1.
SQ SEQUENCE 199 AA; 22150 MW; 401C13EB58CE16 CRC64;

Query Match 53.9%; Score 909; DB 11; Length 199;
Best Local Similarity 85.4%; Pred. No. 4.8e-75;
Matches 170; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 119 IKAQFQAVQKELQHYVSGOHLRAEKAMVDGSMIDLAKRSKLEAOPALHTNATDIPSG 178
DB 1 MKQAFQAVQKELQHYVSGOHLRAEKAMVDGSMIDLAKRSKLEAOPALHTNATDIPSG 60
QY 179 SHKVSLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 238
DB 61 SHKVTLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 120
QY 239 MYYVTKTSIKIPSSHTLMKSGSTKYNSEPHFYSINVGFFKLRSGEISIEVSNPSL 298
DB 121 MYYVTKTSIKIPSSHTLMKSGSTKYNSEPHFYSINVGFFKLRSGEISIEVSNPSL 180
QY 299 LDPDQATYFGAFKVDID 317
DB 181 LDPDQATYFGAFKVDID 199

RESULT 6
Q91ZT9 PRELIMINARY; PRT; 53 AA.
ID Q91ZT9;
AC Q91ZT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TNFSF11 (FRAGMENT).
GN TNFSF11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
OX NCBL_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-F344;
RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C.A., Mason-Savay A.,
RA Safadi F.F., Popoff S.N., Lengner C., van Hul W., Choi Y., Marks S.C.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the Tnfrsf11 (TRANCE, RANKL, ODF, OPG) gene."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF425669; AAL23963.1; -.
FT NON_TER 1
SQ SEQUENCE 53 AA; 5876 MW; 8A71E32F2B6A9410 CRC64;

Query Match 15.5%; Score 262; DB 11; Length 53;
Best Local Similarity 90.6%; Pred. No. 8.3e-17;
Matches 48; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 265 SGNSEPHFYSINVGFFKLRSGEISIEVSNPSLLDPDQATYFGAFKVDID 317
DB 1 SGNSEPHFYSINVGFFKLRSGEISIEVSNPSLLDPDQATYFGAFKVDID 53
RESULT 7
Q9DDZ5 PRELIMINARY; PRT; 214 AA.
ID Q9DDZ5;
AC Q9DDZ5;

| RESULT | 12 |
|--------|--|
| OSM16 | |
| ID | OSM16 |
| AC | PRELIMINARY; |
| DT | 01-OCT-2000 (TREMBlrel, 15, Created) |
| DT | 01-OCT-2000 (TREMBlrel, 15, Last sequence update) |
| DT | 01-DEC-2001 (TREMBlrel, 19, Last annotation update) |
| DE | FAS LIGAND. |
| GN | PT-FASL OR CM-FASL OR RM-FASL. |
| OS | Macaca nemestrina (Pig-tailed macaque), |
| OS | Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and |
| OS | Macaca mulatta (Rhesus macaque) |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Cerepithecidae; |
| OC | Cerepithecinae; Macaca. |
| OX | NCBI_TaxId=9545, 9541, 9544; |
| OX | (1) |
| RN | SEQUENCE FROM N.A. |
| RP | SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY; |
| RC | Kiriti Y., Inoue T., Yoshino K. |

RT "pig-tailed monkey Fas ligand mRNA, complete cds."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA Kiril V., Inoue T., Yoshino K.;
RT "Cynomolgus monkey Fas ligand mRNA, complete cds."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mullatta; STRAIN=RHEBUS MONKEY;
RA Kiril V., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB035140; BAA90296.1; -
DR EMBL: AB035138; BAA90294.1; -
DR EMBL: AB035139; BAA90295.1; -
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISCT.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 11.0%; Score 186; DB 6; Length 280;
Best Local Similarity 22.1%; Pred. No. 7.4e-09;
Matches 69; Conservative 44; Mismatches 103; Indels 96; Gaps 11;

QY 22 PGAPHEGLAHAPPPAP-----HQPAAASR-----MFVALLGLGLGVYCS 63
DB 45 PPPPPPPPLPPPPSPPLPLPLPKKRGKNGSTGLCLVMFVLLVGLGLG----- 99
QY 64 VALFFYFRAQMDPNRISEDTGHCYRILRLHENADPDTTLESQTKLIPDSCRIRKQAF 123
DB 100 --MFOLFHLQ-----KELAELESTSQKHQA----- 123
QY 124 QGAVQKELQHTVSSQHIRAEKAMVDGSLDLAKRSKLEAPFAHLT--INADIPSGSHK 181
DB 124 --SLEKQIGH-----PSPPEKKEQKVAHLTGKPNRSM----- 158
QY 182 VSLSSWYHDGNAKISNMTFSNGKLIVNODGFYUVAICFRHHETSGDLATEYLQIMVY 241
DB 159 ---LEWEDTYGIVLLSGVKKKGGLVINEETGLYFYVSKYVFR---GQSCFN-LPLSHK 209
QY 242 VYKTSIKIPSSHTLMKGGSTKYWSGSEFHFYSINVGCFKLSGGEISIEVSNPSLDP 301
DB 210 VYMRNSKYPQDLYVMEGKMMSYCT--TGQWMAHSSYLGAVFNLISADHLVYVNSLSLVNF 268
QY 302 DDDATYFGAFKV 313
DB 269 EESQTFEGLYKL 280

RESULT 13
Q9BDM5 PRELIMINARY; PRT; 280 AA.
AC Q9BDM5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
NCBI_TaxID=9544;

RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21383618; PubMed-11491535;
RX Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/FasLigand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL: AF344856; AKK37539.1; -
DR HSSP: P01375; 4TSV.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PRINTS: PR01234; TNECROSISCT.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31377 MW; 729EA61436F2D398 CRC64;

Query Match 10.9%; Score 184.5; DB 6; Length 280;
Best Local Similarity 22.4%; Pred. No. 1e-08;
Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

QY 22 PGAPHEGLAHAPPPAPHQP-----AASRS-----MFVALLGLGLGVYCS 62
DB 46 PPPPPPPPL--PPPPPLPLPLPLPKKRGKNGSTGLCLVMFVLLVGLGLG----- 99
QY 63 SVALFFYFRAQMDPNRISEDTGHCYRILRLHENADPDTTLESQTKLIPDSCRIRKQA 122
DB 100 --MFOLFHLQ-----KELAELESTSQKHQA----- 123
QY 123 FQGAVQKELQHTVSSQHIRAEKAMVDGSLDLAKRSKLEAPFAHLT--INADIPSGSH 180
DB 124 --SLEKQIGH-----PSPPEKKEQKVAHLTGKPNRSM----- 158
QY 181 KVSLSWYHDGNAKISNMTFSNGKLIVNODGFYUVAICFRHHETSGDLATEYLQIMVY 240
DB 159 ---LEWEDTYGIVLLSGVKKKGGLVINEETGLYFYVSKYVFR---GQSCFN-LPLSH 208
QY 241 VYKTSIKIPSSHTLMKGGSTKYWSGSEFHFYSINVGCFKLSGGEISIEVSNPSLDP 300
DB 209 KYVMNSKYPQDLYVMEGKMMSYCT--TGQWMAHSSYLGAVFNLISADHLVYVNSLSLVN 267
QY 301 PDDATYFGAFKV 313
DB 268 FEESQTFEGLYKL 280

RESULT 14
Q9BDN1 PRELIMINARY; PRT; 280 AA.
AC Q9BDN1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CD95L PROTEIN.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21383618; PubMed-11491535;
RX Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas-ligand and co-stimulatory molecules";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344847; AAK37606.1; -
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR002965; P-rich_extensn.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR PRINTS: PR01234; TNECROSISCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 SQ SEQUENCE 280 AA; 31407 MW; 729BA60067BD398 CRC64;

Query Match 10.8%; Score 182.5; DB 6; Length 280;
 Best Local Similarity 22.4%; Pred. No. 1.5e-08;
 Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

OY 22 PGAPHGPIHAPPPAPHP-----AASRS-----MFVALLGLGQVVC 62
 DB 46 PPPPPPPPL-PPPPPPPLPLPLPKRGNHSTGLCLLNFVNLVGLGIG---- 99
 OY 63 SVALFFVFAQMDPNRISDGTCHYRIRLHENDFODTLESQDTKLIPSCRIKQA 122
 DB 100 ---MFQLFHLQ-----KELAELESTSGKHTA----- 123
 OY 123 FQCAVQKELQHYVSGHIAEKAMVDGSLDLAKRSKLEAOPFAHLT--INATDIPSGSH 180
 DB 124 ---SSLEKQIGH-----PSPPEKKEQKRVVHLTGKPNRSMP----- 158
 OY 181 KVSLSGMYHDRGMAKISNMTFSGKLIYNQDGFYLYANICFRHNETSGDLATEYLQLMV 240
 DB 159 ----LEMEPTYGIVLLSGYKVKKGLVINETGLFYYSKYVTR-----GQSCTN-LPLSH 208
 OY 241 VYTKTSIKIPSSHLLMKGGSTYRWGSEFNHYSTINVGGEFKLRSGEISIEVSNPSLID 300
 DB 209 KYVMRNSKYPQDLVMEGKMMSYCT-TGQMAHSSYLGAVFNLSTDHLYVVSSELSLVN 267
 OY 301 PQDQATYVGAFKV 313
 DB 268 FEESQTFEGLYKL 280

RESULT 15
 O9BDN3 PRELIMINARY; PRT; 261 AA.
 AC O9BDN3;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CD154 PROTEIN.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
 OX NCBI_TaxID=9483;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas-ligand and co-stimulatory molecules";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344844; AAK37603.1; -
 DR HSSP: P29865; 1ALY.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR000478; TNF_family.

DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 SQ SEQUENCE 261 AA; 29360 MW; 10CA58BD923754EB CRC64;

Query Match 10.1%; Score 169.5; DB 6; Length 261;
 Best Local Similarity 24.6%; Pred. No. 2.1e-07;
 Matches 71; Conservative 55; Mismatches 120; Indels 43; Gaps 15;

OY 33 PPPPAPHOPPARSMPFALLGLG-IGVVCVAFVFFRQMDPNRISDGTCHYRIIL 91
 DB 8 PVPKSAATGPPVSMKIFMLILFVLITOMIGSALFAVYLHRLD--KIEDE-----R 57
 OY 92 RLHENADEFDT--TLESODTKLIPDCRRIKQAFQCAVQKELQHYVSGHIAEKAMVDG 149
 DB 58 NLHEDFVFNMKTQRCNTGERSLSLNCCEIKSQFEGV-KDIM-----LNKEKKKEN 109
 OY 150 SWLDLAKRSKLEAOPFAHLTINATDIPSGSHKVSLSWYHDRGMAKISN--MTFSNCK-L 206
 DB 110 SF-EMQKGDQ-NPQIAAHVISEAS-----SKTTSVLQW-AEKGYTMSNNLVTLKNGKOL 161
 OY 207 IVNQDGFYLYANICFRHNETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTIKY 264
 DB 162 TYKRGGLYIYAQVYFCNREASSAP-----FISLCLKPPNRREBITLLRANAH-- 212
 OY 265 SGNSEFNHYSTINVGGEFKLRSGEISIEVSNPSLIDPQDQATYVGAFKV 313
 DB 213 SSAPKPGQGSIHGLGIFELQPGASVFAVNVTDPSQVSHQGTSTGGLKL 261

Search completed: July 8, 2002, 19:52:38
 Job time: 12582 sec

Tue Jul 9 13:21:07 2002

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